

## Group 5

- SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 1 from Brown provisional No. 1 (60/305,026)

Score = 523 bits (1346), Expect = 6e-146

Identities = 262/398 (65%), Positives = 313/398 (78%), Gaps = 1/398 (0%)

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Query 371 PDLETYNSMIVGFCSSGRWSDAEQLLEMLERKISPDDVVTYNALINAFVKEGKFFAEEL 430
      P++ T+ +++ G C GR +A LL M+E + P+ +TY +++ K G A L
Sbjct 4 PNVVTFITLMNGLCREGRVVEAVALLDRMVEDGLQPNQITYGTIVDGMCKMGDTVSALNL 63

Query 431 YDEMLPRGII-PNTITYSSMIDGFCQNRLDAAEHMFYLMATKGCSPNLITFTNLIDGYC 489
      +M I P+ +YS++IDG K R A+++F M KG P+++T++ +I+G+C
Sbjct 64 LRKMEELSHIKPDVVIYSAIIDGLWKDGRHTDAQNLFIEMQDKGIFPDIVTYSKCMINGFC 123

Query 490 GAKRIDDGMLLHEMTETGLVADTTTYNTLHGFYLVGLDNLAAQLLQEMISSGLCPDIV 549
      + + + LL EM + D T++ LI+ GDLN+A DLLQEMISSG+CP++V
Sbjct 124 SSGKWSEAQRLLEQMLVRKISPDDVVTFSGLINALVKEGDLNSAQLLQEMISSGVCPCNVV 183

Query 550 TCDTLLDGLCDNGKLDKDALEMFVKMQSKKDLDAHPFNGVEPDVQTYNIIISGLINEGK 609
      TC+TLLDGLCD GKLDKDALEMFK MQKS D+DA+H FNGVEPDVQTYNIIISGLINEGK
Sbjct 184 TCDTLLDGLCDRGKLDKDALEMFKAMQSKMMDIDATHAFNGVEPDVQTYNIIISGLINEGK 243

Query 610 FLEAEELYEEMPHRGIVPDTITYSSMIDGLCKQSRLEDEATQMFDMSGKSFSPNVVTFIT 669
      FLEAEELYEEMPHRGIVPDT+TYSSMI+GLCKQSRLEDEATQMFDMSGKSFSPN+VTF T
Sbjct 244 FLEAEELYEEMPHRGIVPDTVITYSSMIDGLCKQSRLEDEATQMFDMSGKSFSPNIVTFNT 303

Query 670 LINGYCKAGRVDDGLELFCMGRRGIVANAITYITLICGFRKVGNGINGALDIFQEMISSG 729
      LI GYCKAG VDDGLELFCMGRRGIVANAITYITLI GFRKVGNGING+LDIFQEMISSG
Sbjct 304 LITGYCKAGVDDGLELFCMGRRGIVANAITYITLIRGFRKVGNGINGSLDIFQEMISSG 363

Query 730 VYPDTITIRNMLTGLWSKEELKRAVAMLEKLQMSMVY 767
      VYPDTITIRNMLTGLWSKEELKRA+AMLE+LQMSMV +
Sbjct 364 VYPDTITIRNMLTGLWSKEELKRALAMLEELQMSMVSF 401
  
```

Score = 394 bits (1012), Expect = 3e-107

Identities = 208/404 (51%), Positives = 265/404 (65%), Gaps = 22/404 (5%)

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Query 263 CRPNVVTFTLMNGLCREGRIVEAVALLDRMMEDGLQPTQITYGTIVDGMCKKGDVTSAL 322
      C+PNVVTFTLMNGLCREGR+VEAVALLDRM+EDGLQP QITYGTIVDGMCK GDTVSA
Sbjct 2 CKPNVVTFTLMNGLCREGRVVEAVALLDRMVEDGLQPNQITYGTIVDGMCKMGDTVSAL 61

Query 323 NLLRKMEEVSHIIPNVVIYSAIIDLCKDGRHSDAQNLFTEMQEKGIFPDFTYNSMIVG 382
      NLLRKME+SHI P+VVIYSAIID L KGRH+DAQNLF EMQ+KGIFPD+ TY+ MI G
Sbjct 62 NLLRKMEELSHIKPDVVIYSAIIDGLWKDGRHTDAQNLFTEMQDKGIFPDIVTYSKCMING 121

Query 383 FCSSGRWSDAEQLLEMLERKISPDDVVTYNALINAFVKEGKFFAEELYDEMLPRGIIPN 442
      FCSSG+WS+A++LLQEML RKISPDDVVT++ LINA VKEG A++L EM+ G+ PN
Sbjct 122 FCSSGKWSAQRLLEMLVRKISPDDVVTFSGLINALVKEGDLNSAQLLQEMISSGVCPCN 181
  
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Query 443 TITYSSMIDGFCQKQNRDLAAEHMFYLM-----ATKGCSPNLITFNTLIDGYCGA 491
      +T ++++DG C + +L A MF M A G P++ T+N LI G
Sbjct 182 VVTCNTLLDGLCDRGKLDKDALEMFKAMQKSMMDIDATHAFNGVEPDVQTYNILISGLINE 241

Query 492 KRIDDGMELLHEMTETGLVADTTTYNTLINGFYLVGDLNAAALLQEMISSGLCPDIVTC 551
      + + EL EM G+V DT TY+++I+G L+ A + M S P+IVT
Sbjct 242 GKFLEAEELYEEMPHRGIVPDTVTYSSMINGLCKQSRLEATQMFDMSGKSFSPNIVTF 301

Query 552 DTLLDGLCDNGKLDKDALEMFKVMQKSKKDL DASHFPNGVEPDVQTYNILISGLINEGKFL 611
      +TL+ G C G + D LE+F M + G+ + TY LI G G
Sbjct 302 NTLITGYCKAGMVDDGLELFCMGR-----RGIVANAITYITLIRGFRKVGNGIN 350

Query 612 EAEELYEEMPHRGIVPDTITYSSMIDGLCKQSRLEATQMFDMS 655
      + ++++EM G+ PDTIT +M+ GL + L A M + +
Sbjct 351 GSLDIFQEMISSGVYPDTITIRNMLTGLWSKEELKRALAMLEEL 394
    
```

Score = 300 bits (767), Expect = 8e-79

Identities = 166/395 (42%), Positives = 229/395 (57%), Gaps = 48/395 (12%)

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Query 230 PDVVTFTLLHGLCVDREVSEALDFFHQMFETTCRPNVVTFTLLMNGLCREGRIVEAVAL 289
      P+VVVFTTL++GLC E RV EA+ +M E +PN +T+ T+++G+C+ G V A+ L
Sbjct 4 PNVVVTFTLLMNGLCREGRVVEAVALLD RMVEDGLQPNQITYGTIVDGMCKMGDTVSALNL 63

Query 290 LDRMME-DGLQPTQITYGTIVDGMCKKGD TVSALNLLRKMEEVSHIIPNVVIYSAIDSL 348
      L +M E ++P + Y I+DG+ K G A NL +M++ I P++V YS +I+
Sbjct 64 LRKMEELSHKPDVVIYSAIDGLWKDGRHTAQNLFIEMQD-KGIFPDIVTYSCHMINGF 122

Query 349 CKDGRHSDAQNLFTEMQEKGIFFPDLFTYNSMIVGFCSSGRWSDAEQLLEMLE----- 401
      C G+ S+AQ L EM + I PD+ T++ +I G + A+ LLQEM+
Sbjct 123 CSSGKWSAQRLLEMLVRKISPDVVTFSGLNALVKEGDLNSAQDLLQEMISSGVCPNV 182

Query 402 -----RKISP DVVTYNALINAFVKEG 422
      + PDV TYN LI+ + EG
Sbjct 183 VTCNTLLDGLCDRGKLDKDALEMFKAMQKSMMDIDATHAFNGVEPDVQTYNILISGLINEG 242

Query 423 KFFEAEELYDEMLPRGIIPNTITYSSMIDGFCQKQNRDLAAEHMFYLMATKGCSPNLITFN 482
      KF EAEELY+EM RGI+P+T+TYSSMI+G CKQ+RLD A MF M +K SPN++TFN
Sbjct 243 KFEAEELYEEMPHRGIVPDTVTYSSMINGLCKQSRLEATQMFDMSGKSFSPNIVTFN 302

Query 483 TLIDGYCGAKRIDDMELLHEMTETGLVADTTTYNTLINGFYLVGDLNAAALLQEMISS 542
      TL L GYC A +DDG+EL EM G+VA+ TY TLI GF VG++N +LD+ QEMISS
Sbjct 303 TLITGYCKAGMVDDGLELFCMGRRGIVANAITYITLIRGFRKVGNGINGSLDIFQEMISS 362

Query 543 GLCPDIVTCDTLLDGLCDNGKLDKDALEMFKVMQKS 577
      G+ PD +T +L GL +LK AL M + +Q S
Sbjct 363 GVPYPTITIRNMLTGLWSKEELKRALAMLEELQMS 397
    
```

## Group 5

Score = 216 bits (551), Expect = 8e-54  
 Identities = 120/392 (30%), Positives = 214/392 (54%), Gaps = 13/392 (3%)

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Query 160 PSVVD FCKLMGVVVRMERPDLVISLYQKMERKQIRCDIYSFNILIKCFCSCSKLPFALST 219
P+VV F LM + R R ++L +M ++ + ++ ++ C AL+
Sbjct 4 PNVVTF T TLMNGLCREGRVVEAVALDRMVEDGLQPNQITYGTIVDGMCKMGDTVSALNL 63

Query 220 FGKITKLGLHPDVVTF T TLLHGLCVEDRVSEALDFHQMFFETTCRPNVVTFT TLMNGLC 278
K+ +L + PDVV ++ ++ GL + R ++A + F +M + P++VT++ ++NG C
Sbjct 64 LRKMEELSHKPDVVIYSAIDGLWKDGRHTDAQNLFIEMQDKGIFPDIVTYS CMINGFC 123

Query 279 REGRIVEAVALDRMMEDGLQPTQITYGTIVDGMCKKGDTSVALNLLRKMEEVSHIIPNV 338
G+ EA LL M+ + P +T+ +++ + K+GD SA +LL+M S + PNV
Sbjct 124 SSGKWSEAQRLLQEMLVRKISPDVVTFSGLINALVKEGDLNSAQDLLQEMIS-SGVCPNV 182

Query 339 VIYSAIDSLCKDGRHSDAQNLFTEMQE-----KGIFPDFTYNSMIVGFCSSG 387
V + ++D LC G+ DA +F MQ+ G+ PD+ TYN +I G + G
Sbjct 183 VTCNTLLDGLCDRGKLDKDALEMFKAMQKSMMDIDATHAFNGVEPDVQTYNILISGLINEG 242

Query 388 RWSDAEQLLQEMLERKISPDVVTYNALINAFVKEGKFFEAELYDEMLPRGIIPNTITYS 447
++ +AE+L +EM R I PD VTY+++IN K+ + EA +++D M + PN +T++
Sbjct 243 KFLAEELYEEMPHRGIVPDTVTYSSMINGLCKQSRLEATQMFDSMGSKFSFSPVITFN 302

Query 448 SMIDGFCQNRDLAAEHMFYLMATKGCSPNLITFNTLIDGYCGAKRIDDGEMELHMETET 507
++I G+CK +D +F M +G N IT+ TLI G+ I+ +++ EM +
Sbjct 303 TLTGYCKAGMVDGLGLEFCFEMGRRGIVANAITYTITLIRGFRKVGNGSLDIFQEMISS 362

Query 508 GLVADTTTYNTLHNGFYLVGDLNALDQLQEM 539
G+ DT T ++ G + +L AL +L+E+
Sbjct 363 GVPDTTITIRNMLTGLWSKEELKRALAMLEEL 394
    
```

Score = 193 bits (491), Expect = 8e-47  
 Identities = 109/371 (29%), Positives = 193/371 (52%), Gaps = 11/371 (2%)

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Query 145 DAIDLFSDMLRSRPLSPVVD FCKLMGVVVRMERPDLVISLYQKMER-KQIRCDIYSFNIL 203
+A+ L M+ P+ + + ++ + +M ++L +KME I+ D+ ++ +
Sbjct 24 EAVALLDRMVEDGLQPNQITYGTIVDGMCKMGDTVSALNLLRKMEEVSHIIPDVVIYSAI 83

Query 204 IKCFCSCSKLPFALSTFGKITKLGLHPDVVTF T TLLHGLCVEDRVSEALDFHQMFFETTC 263
I + A + F ++ G+ PD+VT++ ++G C + SEA +M
Sbjct 84 IDGLWKDGRHTDAQNLFIEMQDKGIFPDIVTYS CMINGFCSSGWSEAQRLLQEMLVRKI 143

Query 264 RPNVVTFT TLMNGLCREGRIVEAVALDRMMEDGLQPTQITYGTIVDGMCKKGDTSVALN 323
P+VVTF+ L+N L +EG + A LL M+ G+ P +T T++DG+C +G AL
Sbjct 144 SPDVVTFSGLINALVKEGDLNSAQDLLQEMISSGVCPNVVTCNTLLDGLCDRGKLDKALE 203

Query 324 LLRKME-----EVSH---IIPNVVIYSAIDSLCKDGRHSDAQNLFTEMQEKGIFPD 373
+ + M+ + +H + P+V Y+ +I L +G+ +A+ L+ EM +GI PD
Sbjct 204 MFKAMQKSMMDIDATHAFNGVEPDVQTYNILISGLINEGKFLAEELYEEMPHRGIVPDT 263
    
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Query 374 FTYNSMIVGFCSSGRWSDAEQLLQEMLERKISPDVVYTINALINAFVKEGKFFFAEELYDE 433
          TY+SMI G C R +A Q+ M + SP++VT+N LI + K G + EL+ E
Sbjct 264 VTYSSMINGLCKQSRLEATQMFDSMGSKSFSPNIVTFNTLITGYCKAGMVDDGLELFCFCE 323

Query 434 MLPRGIIPNTITYSSMIDGFCQNRDLAAEHMFYLMATKGCSPNLITFNTLIDGYCGAKR 493
          M RGI+ N ITY ++I GF K ++ + +F M + G P+ IT ++ G +
Sbjct 324 MGRRGIVANAITYITILIRGFRKVGNGNSLDIFQEMISSGVYPTTITIRNMLTGLWSKEE 383

Query 494 IDDGMEELLHEM 504
          + + +L E+
Sbjct 384 LKRALAMLEEL 394
  
```

Score = 118 bits (296), Expect = 3e-24  
 Identities = 78/282 (27%), Positives = 130/282 (46%), Gaps = 12/282 (4%)

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Query 135 SGFHEIKGLEDAIDLFSMDLRSRPLSPVDFCKLMGVVVRMERPDVLISLYQKMERKQIR 194
          +GF +A L +ML + P VV F L+ +V+ + L Q+M +
Sbjct 120 NGFCSSGKWSEAQRLLQEMLVRKISPDVVTFSGLINALVKEGLNSAQDLLQEMISSGVC 179

Query 195 CDIYSFNILIKCFCSCSKLPFALSTFGKITKL-----GLHPDVVFTTLLHGLC 243
          ++ + N L+ C KL AL F + K G+ PDV T+ L+ GL
Sbjct 180 PNVVTCNLLDGLCDRGKLDALFMFKAMQKSMMDIDATHAFNGVEPDVQYTNILISGLI 239

Query 244 VEDRVSEALDFHQMFEETTCRPNVVFTTLMNGLCREGRIVEAVALDRMMEDGLQPTQI 303
          E + EA + + +M P+ VT+++++NGLC++ R+ EA + D M P +
Sbjct 240 NEGKFLAEELYEEMPHRGIVPDTVTYSSMINGLCKQSRLEATQMFDSMGSKSFSPNIV 299

Query 304 TYGTIVDGCMCKGDTVSALNLLRKMEEVSHIIPNVVIYSALIDSCKDGRHSDAQNLFT 363
          T+ T++ G CK G L L +M I+ N + Y +I K G + + +F E
Sbjct 300 TFNTLITGYCKAGMVDDGLELFCFCEMGRRG-IVANAITYITILIRGFRKVGNGNSLDIFQE 358

Query 364 MQEKGIIPDLFTYNSMIVGFCSSGRWSDAEQLLQEMLERKIS 405
          M G++PD T +M+ G S A +L+E+ +S
Sbjct 359 MISSGVYPTTITIRNMLTGLWSKEELKRALAMLEELQMSMVS 400
  
```

- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 2 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 3 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 4 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found

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- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 5 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 6 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 7 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 8 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 9 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 10 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 11 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 12 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 13 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 14 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 15 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found

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- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 16 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 17 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 18 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 19 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 20 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 21 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 22 from Brown provisional No. 1 (60/305,026)**

Score = 1180 bits (3053), Expect = 0.0  
 Identities = 595/685 (86%), Positives = 629/685 (91%), Gaps = 6/685 (0%)

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Query 84 MLARVCGFKCSSPAESAARLFCTRSIRDTLAKAS--GESCEAGFGGESLKLQSGFHEIK 141
Sbjct 1 MLARVCRTESSSSSSVSARFFCTGSRHALAEKSRDGESGEAGFRGESLKLRSGSYEIK 60

Query 142 GLEDAIDLFSMDLRSRPLPSVDFCKLMGVVVRMERPDVLISLYQKMERKQIRCDIYSFN 201
Sbjct 61 GLEDAIDLFSMDLRSRPLPSVIDFNKLMGAVVRMERPDVLISLYQKMERKQIRCDIYSFT 120

Query 202 ILIKCFCSCKSLPFALSTFGKITKLGLHPDVVTFPTLLHGLCVDREVSEALDFFHQMFT 261
Sbjct 121 ILIKCFCSCKSLPFALSTFGK+TKLGLHPDVVTFPTLLHGLC++RVSEALD FHQ+
177

Query 262 TCRPNVVTFPTLLMNLGCREGRIVEAVALLDRMEDGLQPTQITYGTIVDMCKKGDVTSA 321
Sbjct 178 -CRPDLVTFPTLLMNLGCREGRVVEAVALLDRMVENGLQPDQITYGTIVDMCKMGDTVSA 236
  
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Query	322	LNLLRKMEEVSHIIPNVVIYSAIDSLCKDGRHSDAQNLFTEMQEGKIFPDFTYNSMIV	381
Sbjct	237	LNLLRKMEE+SHIIPNVVIYSAID LCKDGRHSD+ NLF EMQ+KGIFP++ TYN MI	296
Query	382	GFCSSGRWSDAEQLLQEMLERKISPVDVVTYNALINAFVKEGKFFEAELYDEMLPRGIIP	441
Sbjct	297	GFCISGRWSAAQRLQEMLERKISPVDVVTYNALINAFVKEGKFFEAELYDEMLPRGIIP	356
Query	442	NTITYSSMIDGFCQKQNRDLDAEHEMFYLMATKGCSPNLTITNTLIDGYCGAKRIDDMELL	501
Sbjct	357	NTITY+SMIDGFCQ+RLDAE MFYLMATKGCSP++ TF TLIDGYCGAKRIDDMELL	416
Query	502	HEMTETGLVADTTTYNTLIHGFFYLVGDLNAAALDLQEMISSGLCPDIVTCPTLLDGLCDN	561
Sbjct	417	HEMPRRGLVANTVTYNTLIHGFFYLVGDLNAAALDLQEMISSGVCPIVTCPTLLDGLCDN	476
Query	562	GKLDKDALEMFQVMQKSKKDLDAHPFNGVEPDVQTYNIIISGLINEGKFLAEELYEEMP	621
Sbjct	477	GKLDKDALEMFQVMQKSK DLDASHPFNGVEPDV TYNII GLINEGKFLAEELYEEMP	536
Query	622	HRGIVPDTITYSSMIDGLCKQSRLEATQMFDSMGSKSFSPNVVTTTLINGYCKAGRVD	681
Sbjct	537	HRGIVPDTITYSSMIDGLCKQSRLEATQMF SMGSKSFSPNVVTF TLINGYCKAGRVD	596
Query	682	DGLELFCCEMGRRGIVANAITYITLICGFRKVGNGINGALDIFQEMISSGVYPDTITIRNML	741
Sbjct	597	DGLELFCCEMGRRGIVA+AI YITLI GFRKVGNGINGALDIFQEMISSGVYPDTITIRNML	656
Query	742	TGLWSKEELKRAVAMLEKLQMSMVY 766	
Sbjct	657	TG WSKEEL+RAVAMLE LQMS+ Y	
		TGFWSKEELERAVAMLEDLQMSVGY 681	

- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 23 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 24 from Brown provisional No. 1 (60/305,026)**

Score = 1624 bits (4206), Expect = 0.0  
 Identities = 804/804 (100%), Positives = 804/804 (100%), Gaps = 0/804 (0%)

Query	1	MEAPNYPPIFFGLNLGVPLEGGRSGTYSGFGSSLFGRIFGVKDFSPIRLFLNYGSGSVRI	60
Sbjct	1	MEAPNYPPIFFGLNLGVPLEGGRSGTYSGFGSSLFGRIFGVKDFSPIRLFLNYGSGSVRI	60
Query	61	LADSSRVFFDRRRRTKFRNKNKMLARVCGFKCSSSPAESAARLFCSTRSIRDTLAKASGE	120
Sbjct	61	LADSSRVFFDRRRRTKFRNKNKMLARVCGFKCSSSPAESAARLFCSTRSIRDTLAKASGE	120

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Query	121	SCEAGFGGESLKLQSGFHEIKGLEDAIDLFSMDLSRSLPSVVDCKLMGVVVRMERPD	180
		SCEAGFGGESLKLQSGFHEIKGLEDAIDLFSMDLSRSLPSVVDCKLMGVVVRMERPD	
Sbjct	121	SCEAGFGGESLKLQSGFHEIKGLEDAIDLFSMDLSRSLPSVVDCKLMGVVVRMERPD	180
Query	181	VISLYQKMERKQIRCDIYSPNLIKCFSCSKLPALSTFGKITKGLHLPDVVFTTLLH	240
		VISLYQKMERKQIRCDIYSPNLIKCFSCSKLPALSTFGKITKGLHLPDVVFTTLLH	
Sbjct	181	VISLYQKMERKQIRCDIYSPNLIKCFSCSKLPALSTFGKITKGLHLPDVVFTTLLH	240
Query	241	GLCVEDRVSEALDFFHQMFETTCRPNVVTFTTLMNGLCREGRIVEAVALDRMMEDGLQ	300
		GLCVEDRVSEALDFFHQMFETTCRPNVVTFTTLMNGLCREGRIVEAVALDRMMEDGLQ	
Sbjct	241	GLCVEDRVSEALDFFHQMFETTCRPNVVTFTTLMNGLCREGRIVEAVALDRMMEDGLQ	300
Query	301	TQITYGTIVDMCKKGGDTVSALNLLRKMEEVSHIIPNVVIYSAIDSLCKDGRHSDAQN	360
		TQITYGTIVDMCKKGGDTVSALNLLRKMEEVSHIIPNVVIYSAIDSLCKDGRHSDAQN	
Sbjct	301	TQITYGTIVDMCKKGGDTVSALNLLRKMEEVSHIIPNVVIYSAIDSLCKDGRHSDAQN	360
Query	361	FTEMQEKGIFFDLFTYNSMIVGFCSSGRWSDAEQLLOEMLERKISPDDVTYNALINAFVK	420
		FTEMQEKGIFFDLFTYNSMIVGFCSSGRWSDAEQLLOEMLERKISPDDVTYNALINAFVK	
Sbjct	361	FTEMQEKGIFFDLFTYNSMIVGFCSSGRWSDAEQLLOEMLERKISPDDVTYNALINAFVK	420
Query	421	EGKFFEAEELYDEMLPRGIIIPNTITYSSMIDGFCQKQNRDLAAEHMFYLMATKGCSPN	480
		EGKFFEAEELYDEMLPRGIIIPNTITYSSMIDGFCQKQNRDLAAEHMFYLMATKGCSPN	
Sbjct	421	EGKFFEAEELYDEMLPRGIIIPNTITYSSMIDGFCQKQNRDLAAEHMFYLMATKGCSPN	480
Query	481	FNTLDIGYCGAKRIDDGMELLHEMTETGLVADTTTYNTLHGFIYLVGDLNAAALDQLQ	540
		FNTLDIGYCGAKRIDDGMELLHEMTETGLVADTTTYNTLHGFIYLVGDLNAAALDQLQ	
Sbjct	481	FNTLDIGYCGAKRIDDGMELLHEMTETGLVADTTTYNTLHGFIYLVGDLNAAALDQLQ	540
Query	541	SSGLCPDIVTCDTLLDGLCDNGKLDKDALEMFKVMQSKKDLDAHPFNFGVEPVDQTYN	600
		SSGLCPDIVTCDTLLDGLCDNGKLDKDALEMFKVMQSKKDLDAHPFNFGVEPVDQTYN	
Sbjct	541	SSGLCPDIVTCDTLLDGLCDNGKLDKDALEMFKVMQSKKDLDAHPFNFGVEPVDQTYN	600
Query	601	ISGLINEGKFLAEAEELYEMPFRGIVPDTITYSSMIDGLCKQSRLEATQMFDSMGSKSF	660
		ISGLINEGKFLAEAEELYEMPFRGIVPDTITYSSMIDGLCKQSRLEATQMFDSMGSKSF	
Sbjct	601	ISGLINEGKFLAEAEELYEMPFRGIVPDTITYSSMIDGLCKQSRLEATQMFDSMGSKSF	660
Query	661	SPNVVFTTTLINGYCKAGRVDDGLELFCMGRRGIVANAIITYITLICGFRKVGNGINGAL	720
		SPNVVFTTTLINGYCKAGRVDDGLELFCMGRRGIVANAIITYITLICGFRKVGNGINGAL	
Sbjct	661	SPNVVFTTTLINGYCKAGRVDDGLELFCMGRRGIVANAIITYITLICGFRKVGNGINGAL	720
Query	721	IFQEMISSGVYPTITIRNMLTGLWSKEELKRAVAMLEKLQMSMVYVWSELKRHTFQKIS	780
		IFQEMISSGVYPTITIRNMLTGLWSKEELKRAVAMLEKLQMSMVYVWSELKRHTFQKIS	
Sbjct	721	IFQEMISSGVYPTITIRNMLTGLWSKEELKRAVAMLEKLQMSMVYVWSELKRHTFQKIS	780
Query	781	GVKRCLGVCPCFSCCHGYRQARSS 804	
		GVKRCLGVCPCFSCCHGYRQARSS	
Sbjct	781	GVKRCLGVCPCFSCCHGYRQARSS 804	

- SEQ 3 from Japanese application from April 2001 (JP 2001-128000) against PRT SEQ 25 from Brown provisional No. 1 (60/305,026)



## Group 5

Score = 975 bits (2521), Expect = 0.0

Identities = 511/690 (74%), Positives = 569/690 (82%), Gaps = 48/690 (6%)

Query	84	MLARVCGFKCSSPAESARLFCTRSIRDTLAKASGESCEAGFGGESLKLQSGFHEIKGL	143
		MLARV SSSPA SAARLFCTRSIR LAK S + E+GFGGESLKL+SGFHEIKGL	
Sbjct	1	MLARVYRSGSSSPAVSAARLFCTRSIRHALAKKSRDG-ESGFGGESLKLRSQGFHEIKGL	59
Query	144	EDAIDLFSMDLRSRPLPSVDFCKLMGVVVRMERPDVLVISLYQKMERKQIRCDIYSFNIL	203
		EDAIDL F DM+RSRPLPSV+DFCKLMGVVVRM R D+VISL++KME +++ C+ YSF IL	
Sbjct	60	EDAIDLFDMVRSRPLPSVIDFCKLMGVVVRMRDLVVVISLHRKMEMRRVPCNAYSFTIL	119
Query	204	IKCFCSCKLFPALSTFGKITKGLHDPVVTFTLLHGLCVDREVSEALDFHQMFFETTC	263
		+KCFCSCKLFPALSTFGKITKGL FH	
Sbjct	120	MKCFCSCKLFPALSTFGKITKLG-----FH-----	145
Query	264	RPNVVTFTTLMNGLCREGRIVEAVALDRMMEDGLQPTQITYGTIVDGMCKKGDVTSALN	323
		P VVTF+TL++GLC E RI EA+ L +M + P +T+ T++G+C++G V A+	
Sbjct	146	-PTVTFSTLLHGLCVDREISALDLFHQMCK---PNVVTFTTLMNGLCREGRIVEAVA	200
Query	324	LLRKMEEVSHIIPNVVVISAIIDSLCKDGRHSDAQNLFTEMQEGK-IFPDLFITY-----	377
		LL +M E + PN + Y I+D +CK G A NL +M+E I P++ +	
Sbjct	201	LLDRMLE-DGLQPNQITYGTIVDGMCKMGDTVSALNLLRKMEEVSHIKPNVVIWPLERRT	259
Query	378	SMIVGFCSSGRWSDAEQLQEMLERK-ISPDPVVTYNALINAFVKEGKFFAEELYDEMPL	436
		M I GFCSSGRWS+A+QLQEMLERK ISPDPVVTYNALINAFVKEGKFFAEELYDEMPL	
Sbjct	260	CMINGFCSSGRWSEAQQLQEMLERKKISPDPVVTYNALINAFVKEGKFFAEELYDEMPL	319
Query	437	RGIIPNTITYSSMIDGFCQKQNRDLAAEHMFYLMATKGCSPNLTFTNLIDGYCGAKRID	496
		RGIIP+TITYSSMIDGFCQKQNRDLAAEHMFYLMATKGCSP++ITFTNLI GYC AKR+DD	
Sbjct	320	RGIIPSTITYSSMIDGFCQKQNRDLAAEHMFYLMATKGCSPDIITFTNLIAGYCRAKRVDD	379
Query	497	GMEILLHMETETGLVADTTTYNTLIHGFLYVGLDNLAAQLQEMISSGLCPDITVCDTLLD	556
		G++LLHMETE GLVA+T TY TLIHGF VGLDNLAA DLLQEM+SSG+CP++VTC+TLLD	
Sbjct	380	GIKLLHMETEAGLVANTITYTTTLIHGFCQVGLDNLAAQLQEMVSSGVCPPNVVTCNTLLD	439
Query	557	GLCDNGKLKDALEMFKVMQSKKDLDSHPFNGVEPDVQTYNINISGLINEGKFLEAEEL	616
		GLCDNGKLKDALEMFK MQSK D+DASHPFNGVEPDVQTYNINISGLINEGKFLEAEEL	
Sbjct	440	GLCDNGKLKDALEMFKAMQSKMDIDASHPFNGVEPDVQTYNINISGLINEGKFLEAEEL	499
Query	617	YEEMPHRGIVPDTITYSSMIDGLCKQSRLEDEATQMFDSMGSKSFSPPNVVFTTTLINGYCK	676
		YEEMPHRGIVPDTITY+S+I GLCKQSRLEDEATQMFDSMGSKSFSPPNVVFTTTLINGYCK	
Sbjct	500	YEEMPHRGIVPDTITYNSVINGLCKQSRLEDEATQMFDSMGSKSFSPPNVVFTTTLINGYCK	559
Query	677	AGRVDDGLELFCMGRRGIVANAITTYITLIGFRKVGNGINGALDIFQEMISSGVYPDIT	736
		AGRVDDGLELFCMGRRGIVANAITTYITL GFRKVGNGINGALDIFQEM++SGVYPDIT	
Sbjct	560	AGRVDDGLELFCMGRRGIVANAITTYITLIHGFRKVGNGINGALDIFQEMASGVYPDIT	619
Query	737	IRNMLTGLWSKEELKRAVAMLEKLQMSMVY 766	
		IRNMLTGLWSKEELKRAVAMLE LQMS+ Y	
Sbjct	620	IRNMLTGLWSKEELKRAVAMLEDLQMSVGY 649	

## Group 5

- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 26 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 27 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 28 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 29 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 30 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 31 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 32 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 33 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 34 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 35 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 36 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found

## Group 5

- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 37 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 38 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 39 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 40 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 41 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against SEQ 4 from Brown provisional No. 2 (60/305,363)**

Score = 1180 bits (3053), Expect = 0.0

Identities = 595/685 (86%), Positives = 629/685 (91%), Gaps = 6/685 (0%)

```

Query 84 MLARVCGFKCSSPAESARLFCTRSIRDTLAKAS--GESCEAGFGGESLKLQSGFHEIK 141
          MLARVC F+ SSS + SAAR FCT SIR LA+ S GES EAGF GESLKL+SG +EIK
Sbjct 1 MLARVCRFESSSSSVSAARFFCTGSIRHALAEKSRDGESEAGFRGESLKLRSGSYEIK 60

Query 142 GLEDAIDLFSDMLRSRPLPSVVD FCKLMGVVVRMERPDVLISLYQKMERKQIRCDIYSFN 201
          GLEDAIDLFSDMLRSRPLPSV+DF KLMG VVRMERPDVLISLYQKMERKQIRCDIYSF
Sbjct 61 GLEDAIDLFSDMLRSRPLPSVIDFNKLMGAVVRMERPDVLISLYQKMERKQIRCDIYSFT 120

Query 202 ILIKCFCSCKSLPFALSTFGKITKLGLHPDVVTFPTLLHGLCVDREVSEALDFFHQMFET 261
          ILIKCFCSCKSLPFALSTFGK+TKLGLHPDVVTFPTLLHGLC++ RVSEALD FHQ+
Sbjct 121 ILIKCFCSCKSLPFALSTFGKLTKLGLHPDVVTFPTLLHGLCLDHRVSEALDLFHQI--- 177

Query 262 TCRPNVVVTFPTLLMNGLCREGRIVEAVALLDRMEDGLQPTQITYGTIVDGMCKKGDVTSA 321
          CRP+V+TFPTLLMNGLCREGR+VEAVALLDRM+E+GLQP QITYGT VDGCK GDVTSA
Sbjct 178 -CRPDVLTFTPTLLMNGLCREGRVVEAVALLDRMVENGLQPDQITYGTIVDGMCKKGDVTSA 236

Query 322 LNLLRKMEEVSHIIPNVVIYSAIDSLCKDGRHSDAQNLFTEMOEKGFPPDLFTYNSMIV 381
          LNLLRKMEE+SHI PNVVIYSAID LCKDGRHSD+ NLF EMQ+KGIFP++ TYN MI
Sbjct 237 LNLLRKMEEISHIKPNVVIYSAIDGLCKDGRHSDSHNLFEMQDKGIFPPIVITYNCMIG 296
  
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## Group 5

Query	382	GFCSSGRWSDAEQLLQEMLERKISPDVVYTNALINAFVKEGKFFEAELYDEMLPRGIIP	441
Sbjct	297	GFC SGRWS A++LLQEMLERKISP+VVYTNALINAFVKEGKFFEA ELYDEMLPRGIIP	356
Query	442	NTITYSSMIDGFCCKQNRDLAAEHMFYLMATKGCSPLNLTFTNTLIDGYCGAKRIDDMELL	501
Sbjct	357	NTITY+SMIDGFCCK+RLDAAE MFYLMATKGCS++ TF TLIDGYCGAKRIDDMELL	416
Query	502	HEMTETGLVADTTTTYNTLHGFYLVGDLNAAALDLQEMISSGLCPDIVTCNTLLDGLCDN	561
Sbjct	417	HEMPRRGLVANTVYNTLHGFCLVGLNAAALDLQ+MISSG+CPDIVTC+TLLDGLCDN	476
Query	562	GKLKDALEMFVKMQSKKDLDAHPFNGVEPDVQTYTNILISGLINEGKFLAEELYEEMP	621
Sbjct	477	GKLKDALEMPK MQSK DLDASHPFNGVEPDV TYNILI GLINEGKFLAEELYEEMP	536
Query	622	HRGIVPDTITYSSMIDGLCKQSRLEATQMFDSMGSKSFPNVVFTTTLINGYCKAGRVD	681
Sbjct	537	HRGIVPDTITYSSMIDGLCKQSRLEATQMF SMGSKSFPNVVTF TLINGYCKAGRVD	596
Query	682	DGLELFCEMGRRGIVANAITYITLICGFRKVGNGINGALDIFQEMISSGVYPTITIRNML	741
Sbjct	597	DGLELFCEMGRRGIVAAIYITLIYGRKVGNGINGALDIFQEMISSGVYPTITIRNML	656
Query	742	TGLWSKEELKRAVAMLEKLQMSVY 766	
Sbjct	657	TG WSKEEL+RAVAMLE LQMS+ Y	681

- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against SEQ 5 from Brown provisional No. 2 (60/305,363)**

Score = 1624 bits (4206), Expect = 0.0

Identities = 804/804 (100%), Positives = 804/804 (100%), Gaps = 0/804 (0%)

Query	1	MEAPNYPPIFFGLNLGVPLEGGRSGTYSGFGSSLFGFRIFGVKDFSPIRLFLNYGSGSVRI	60
Sbjct	1	MEAPNYPPIFFGLNLGVPLEGGRSGTYSGFGSSLFGFRIFGVKDFSPIRLFLNYGSGSVRI	60
Query	61	LADSSRVFFRRRRRTKFRNKNKMLARVCGFKCSSSPAESAARLFCTRSIRDTLAKASGE	120
Sbjct	61	LADSSRVFFRRRRRTKFRNKNKMLARVCGFKCSSSPAESAARLFCTRSIRDTLAKASGE	120
Query	121	SCEAGFGGESLKLQSGFHEIKGLEDAIDLFSMDLSRPLSPVVDCKLMGVVVRMERPD	180
Sbjct	121	SCEAGFGGESLKLQSGFHEIKGLEDAIDLFSMDLSRPLSPVVDCKLMGVVVRMERPD	180
Query	181	VISLYQKMERKQIRCDIYSFNILIKCFCSCSKLPALSTFGKITKLGLHPDVVFTTTLH	240
Sbjct	181	VISLYQKMERKQIRCDIYSFNILIKCFCSCSKLPALSTFGKITKLGLHPDVVFTTTLH	240

## Group 5

Query	241	GLCVEDRVSEALDFHQMFEETTCRPNVVFTTLMNGLCREGRIVEAVALLDRMMEDGLQP	300
Sbjct	241	GLCVEDRVSEALDFHQMFEETTCRPNVVFTTLMNGLCREGRIVEAVALLDRMMEDGLQP	300
Query	301	TQITYGTIVDMCKKGDTSALNLLRKMEEVSHIIPNVVIYSATIDSLCKDGRHSDAQNL	360
Sbjct	301	TQITYGTIVDMCKKGDTSALNLLRKMEEVSHIIPNVVIYSATIDSLCKDGRHSDAQNL	360
Query	361	FTEMQEKGIFFDLFTTNSMIVGFCSSGRWSDAEQLLOEMLERKISPDVVTYNALINAFVK	420
Sbjct	361	FTEMQEKGIFFDLFTTNSMIVGFCSSGRWSDAEQLLOEMLERKISPDVVTYNALINAFVK	420
Query	421	EGKFFAEELYDEMLPRGIIPNTITYSSMIDGFCKQNRDLAAEHMFYLMATKGCSPNLIT	480
Sbjct	421	EGKFFAEELYDEMLPRGIIPNTITYSSMIDGFCKQNRDLAAEHMFYLMATKGCSPNLIT	480
Query	481	FNTLIDGYCGAKRIDGMEHMETETGLVADTTTYNTLHGFYLVGDLNAAALLQEMI	540
Sbjct	481	FNTLIDGYCGAKRIDGMEHMETETGLVADTTTYNTLHGFYLVGDLNAAALLQEMI	540
Query	541	SSGLCPDIVTCDTLLDGLCDNGKLKDALEMFKVMQSKSKDLDAHPFNGVEPVDQTYNIL	600
Sbjct	541	SSGLCPDIVTCDTLLDGLCDNGKLKDALEMFKVMQSKSKDLDAHPFNGVEPVDQTYNIL	600
Query	601	ISGLINEGKFLAEELYEEMPHRGIVPDTITYSSMIDGLCKQSRLEATQMFDSMGSKSF	660
Sbjct	601	ISGLINEGKFLAEELYEEMPHRGIVPDTITYSSMIDGLCKQSRLEATQMFDSMGSKSF	660
Query	661	SPNVVFTTTLINGYCKAGRVDDGLELFCMGRRGIVANAIITYITLCGRKRVGNINGALD	720
Sbjct	661	SPNVVFTTTLINGYCKAGRVDDGLELFCMGRRGIVANAIITYITLCGRKRVGNINGALD	720
Query	721	IFQEMISSGVYPDTITIRNMLTGLWSKEELKRAVAMLEKLQMSMVVYWSSELKRHTFQKIS	780
Sbjct	721	IFQEMISSGVYPDTITIRNMLTGLWSKEELKRAVAMLEKLQMSMVVYWSSELKRHTFQKIS	780
Query	781	GVKRCLGVCPCFSCCHHGVRQARSS 804	
Sbjct	781	GVKRCLGVCPCFSCCHHGVRQARSS 804	

- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against SEQ 6 from Brown provisional No. 2 (60/305,363)**

Score = 975 bits (2521), Expect = 0.0  
 Identities = 511/690 (74%), Positives = 569/690 (82%), Gaps = 48/690 (6%)

Query	84	MLARVCGFKCSPSPAESARLFCTRSIRDTLAKASGESCEAGFGGESLKLQSGFHEIKGL	143
Sbjct	1	MLARVYRSGSSSPAVSARLFCTRSIRHALAKKSRDG-ESGFGGESLKLRSGFHEIKGL	59

## Group 5

Query	144	EDAIDLFSMDLRSRPLPSVDFCKLMGVVVRMERPDVLISLYQKMERKQIRCDIYSEFNIL	203
Sbjct	60	EDAIDLFDGDMVRSRPLPSVDFCKLMGVVVRMRGLDVVISLHRKMEVRVPCNAYSFTIL	119
Query	204	IKCFCSCSKLPALSTFGKITKGLHPDVVTFITLLHGLCEDRVSEALDFFHQMFETTC	263
Sbjct	120	IKCFCSCSKLPALSTFGKITKGL-----FH-----	145
Query	264	RPNVVFITLLMNGLCREGRIVEAVALDRMMEDGLQPTQITYGTIVDGMCKKGDTVSALN	323
Sbjct	146	P VVTF+TL++GLC E RI EA+ L +M + P +T+ T+++G+C++G V A+ -PTVTFSTLLHGLCEDRVSEALDLTHQMCK---PNVVFITLLMNGLCREGRVVEAVA	200
Query	324	LLRKMEEVSHIIPNVVIYSIIIDSLCKDGRHSDAQNLFTEMQKQG-IFPDFTTY-----N	377
Sbjct	201	LL +M E + PN + Y I+D +CK G A NL +M+E I P++ + LLDRMLE-DGLQPNQITYGTIVDGMCKKGDTVSALNLLRKMEEVSHIKPNVVIWPLERRT	259
Query	378	SMIVGFCSSGRWSDAEQLQOEMLERK-ISPDDVVTYNALINAFVKEGKFFEAEEELYDEMPL	436
Sbjct	260	MZ GFCSSGRWS+A+QLQOEMLERK ISPDDVVTYNALINAFVKEGKFFEAEEELYDEMPL CMINGFCSSGRWSEAQLQOEMLERKKISPDDVVTYNALINAFVKEGKFFEAEEELYDEMPL	319
Query	437	RGIIPNTITYSSMIDGFCQKQNRDLAAEHMFYLMATKGCSPNLTITNTLIDGYCGAKRID	496
Sbjct	320	RGIIPNTITYSSMIDGFCQKQNRDLAAEHMFYLMATKGCSPDIITNTLTIAGYCRAKRVDD	379
Query	497	GMELLHEMTETGLVADTTTYNTLHGFYLVGDLNAAQLLQEMISSGLCPDIVTCDTLLD	556
Sbjct	380	G++LLHEMT E GLVA+T TY TLHGF VGDNLAA DLLQEM+SSG+CP++VTC+TLLD GIKLLHEMT EAGLVANTITYNTLHGFQVGDNLAAQDLLQEMVSSGVCNPNVVTCTLLD	439
Query	557	GLCDNGKLKDALEMFVKMOKSKKDLDDASHFPNGVEPDVQTYNINISGLINEGKFLEAEEL	616
Sbjct	440	GLCDNGKLKDALEMFK MOKSK D+DASHFPNGVEPDVQTYNINISGLINEGKFLEAEEL GLCDNGKLKDALEMFKAMOKSKMDIDASHFPNGVEPDVQTYNINISGLINEGKFLEAEEL	499
Query	617	YEEMPHRGIVPDTITYSSMIDGLCKQSRLEATQMFDSMGSKSFSPNVVTFITTLINGYCK	676
Sbjct	500	YEEMPHRGIVPDTITY+S-I GLCKQSRLEATQMFDSMGSKSFSPNVVTFITTLINGYCK YEEMPHRGIVPDTITYNSVIHGLCKQSRLEATQMFDSMGSKSFSPNVVTFITTLINGYCK	559
Query	677	AGRVDDGLELFCMGRRGIVANAITYITLICGRKVGNGINGALDIFQEMISSGVYPDTIT	736
Sbjct	560	AGRVDDGLELFCMGRRGIVANAITYITLIHGRKVGNGINGALDIFQEM+SGVYPDTIT AGRVDDGLELFCMGRRGIVANAITYITLIHGRKVGNGINGALDIFQEMMASGVYPDTIT	619
Query	737	IRNMLTGLWSKEELKRAVAMLEKLQMSMVY	766
Sbjct	620	IRNMLTGLWSKEELKRAVAMLE LQMS+ Y IRNMLTGLWSKEELKRAVAMLEDLQMSVG Y	649

- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 1 from Brown provisional No. 3 (60/308,736)**

Score = 523 bits (1346), Expect = 6e-146  
 Identities = 262/398 (65%), Positives = 313/398 (78%), Gaps = 1/398 (0%)

## Group 5

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Query 371 PDLETYNSMIVGFCSSGRWSDAEQLLQOEMLERKISPDDVVTYNALINAFVKEGKFFAEAEEL 430
      P++ T+ +++ G C GR +A LL M+E + P+ +TY +++ K G A L
Sbjct 4 PNVVTTTTLNGLCREGRVVEAVALLDRMVEDGLQPNQITYGTIVDGMCKMGDTVSALNL 63

Query 431 YDEMLPRGII-PNTITYSSMIDGFCQNRDLAAEHMFYLMATKGCSPNLITFNTLIDGYC 489
      +M I P+ + YS++IDG K R A+++F M KG P+++T++ +I+G+C
Sbjct 64 LRKMEELSHIKPDVVIYSATIDGLWKDGRHTDAQNLFIEMQDKGIFPDIVTYSKMGFC 123

Query 490 GAKRIDDMGELLHEMTETGLVADTTTYNTLHGFYLVGLDNLAAALDLLOEMISSGLCPDIV 549
      + + + LL EM + D T++ LI+ GDLN+A DLLQOEMISSG+CP++V
Sbjct 124 SSGKWSEAQRLLOQEMLVKISPDDVVTFSGLINALVKEGDLNSAQDLLOEMISSGVCNVV 183

Query 550 TCDTLLDGLCDNGKLDKDALEMFVKMQSKKDLDAHPFNGVEPDVQTYNINISGLINEGK 609
      TC+TLLDGLCD GKLDKDALEMFK MQKS D-DA+H FNGVEPDVQTYNINISGLINEGK
Sbjct 184 TCNTLLDGLCDRGKLDKDALEMFKAMQSKMMDIDATHAFNGVEPDVQTYNINISGLINEGK 243

Query 610 FLEAEELYEEMPHRGIVPDTITYSSMIDGLCKQSRLEATQMFDSMGSKSFSPNVVTF 669
      FLEAEELYEEMPHRGIVPDT+TYSSMI+GLCKQSRLEATQMFDSMGSKSFSPN+VTF T
Sbjct 244 FLEAEELYEEMPHRGIVPDTVITYSSMIDGLCKQSRLEATQMFDSMGSKSFSPNIVTF 303

Query 670 LINGYCKAGRVDDGLELFCMGRRGIVANAITYITLICGRKVGNGINGALDIFQOEMISSG 729
      LI GYCKAG VDDGLELFCMGRRGIVANAITYITLI GFRKVGNGING+LDIFQOEMISSG
Sbjct 304 LITGYCKAGRVDDGLELFCMGRRGIVANAITYITLIRKVGNGINGSLDIFQOEMISSG 363

Query 730 VYPDTITIRNMLTGLWSKEELKRAVAMLEKLQMSMVY 767
      VYPDTITIRNMLTGLWSKEELKRA+AMLE+LQMSMV +
Sbjct 364 VYPDTITIRNMLTGLWSKEELKRALAMLEELQMSMVSF 401

Score = 394 bits (1012), Expect = 3e-107
Identities = 208/404 (51%), Positives = 265/404 (65%), Gaps = 22/404 (5%)

Query 263 CRPNVVTFTTLNGLCREGRIVEAVALLDRMMEDGLQPTQITYGTIVDGMCKKGDTSAL 322
      C+PNVVTFTTLNGLCREGR+VEAVALLDRM+EDGLQPT QITYGTIVDGMCK GDTSAL
Sbjct 2 CKPNVVTFTTLNGLCREGRVVEAVALLDRMVEDGLQPNQITYGTIVDGMCKMGDTVSAL 61

Query 323 NLLRKMEEVSHIIPNVVIYSATIDSLCKDGRHSDAQNLFTEMQEKGIFPDFTYNSMIVG 382
      NLLRKME+SHI P+VVIYSATID L KDGRH+DAQNLF EMQ+KGIFPD+ TY+ MI G
Sbjct 62 NLLRKMEELSHIKPDVVIYSATIDGLWKDGRHTDAQNLFIEMQDKGIFPDIVTYSKMG 121

Query 383 FCSSGRWSDAEQLLQOEMLERKISPDDVVTYNALINAFVKEGKFFAEAEELYDEMLPRGIIPN 442
      FCSSG+WS+A++LLQOEM RLISPDDV++ LINA VKEG A++L EM+ G+ PN
Sbjct 122 FCSSGKWSEAQRLLOQEMLVKISPDDVVTFSGLINALVKEGDLNSAQDLLOEMISSGVCNP 181

Query 443 TITYSSMIDGFCQNRDLAAEHMFYLM-----ATKGCSPNLITFNTLIDGYCGA 491
      +T ++++DG C + +L A MF M A G P++ T+N LI G
Sbjct 182 VVTCNTLLDGLCDRGKLDKDALEMFKAMQSKMMDIDATHAFNGVEPDVQTYNINISGLINE 241

Query 492 KRIDDGMELLHEMTETGLVADTTTYNTLHGFYLVGLDNLAAALDLLOEMISSGLCPDIVTC 551
      + + EL EM G+V DT TY+++I+G L+ A + M S P+IVT
Sbjct 242 GKFLAEAEELYEEMPHRGIVPDTVITYSSMIDGLCKQSRLEATQMFDSMGSKSFSPNIVTF 301

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## Group 5

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Query 552 DTLLDGLCDNGKLDKDALEMFKVMQKSKDL DASHPFNGVPEPDVQTYNIIISGLINEGKFL 611
+TL+ G C G + D LE+F M + G+ + TY LI G G
Sbjct 302 NTLITGYCKAGMVDDGLLFCCEMGR-----RGIVANAITYITLIRGFRKVGNN 350

Query 612 EAEELYEEMPHRGIVPDTTITYSSMIDGLCKQSRLEATQMFDSM 655
+ ++++EM G+ PDTIT +M+ GL + L A M + +
Sbjct 351 GSLDIFQEMISSGVYPTTITIRNMLTGLWSKEELKRALAMLEEL 394
  
```

Score = 300 bits (767), Expect = 8e-79  
 Identities = 166/395 (42%), Positives = 229/395 (57%), Gaps = 48/395 (12%)

```

Query 230 PDVVTFTTLLHGLCVEDRVSEALDFHQMFEETTCRPNVVTFTTLMNGLCREGRIVEAVAL 289
P+VVTFPTL++GLC E RV EA+ +M E +PN +T+ T+++G+C+ G V A+ L
Sbjct 4 PNVVTFPTLMMNGLCREGRVVEAVALDRMVEDGLQPNQITYGTIVDGMCKMGDTVSALNL 63

Query 290 LDRMME-DGLQPTQITYGTIVDGMCKKGDTSVALNLLRKMEEVSHIIPNVVYISAIDSL 348
L +M E ++P + Y I+DG+ K G A NL +M++ I P++V YS +I+
Sbjct 64 LRKMEELSHIKPDVVYISAIDGLWKDGRHTDAQNLFIEMQD-KGIFPDIVTYSCHINGF 122

Query 349 CKDGRHSDAQNLFTMEQEKGIFPDFTYNSMIVGFCSSGRWSDAEQLLQEMLE----- 401
C G+ S+AQ L EM + I PD+ T++ +I G + A+ LLQEM+
Sbjct 123 CSSGKWSAEARLLQEMLVKRISPDVVTFSGLINALVKEGDLNSAQDLLQEMISSGVCNV 182

Query 402 -----RKISPVDVVTYNALINAFVKEG 422
+ PDV TYN LI+ + EG
Sbjct 183 VTCNTLLDGLCDRGLKDALEMFKAMQKSMMDIDATHAFNGVPEPDVQTYNIIISGLINEG 242

Query 423 KFEAEELYDEMLPRGIIPNTITYSSMIDGFCCKQNRDLAAEHMFYLMATKGCSPNLITFN 482
KF EAEELY+EM RGI+P+T+TYSSMI+G CKQ+RLD A MF M +K SPN++TFN
Sbjct 243 KFLAEELYEEMPHRGIVPDTVTYSSMINGLCKQSRLEATQMFDSMGSKSFSFNIVTFN 302

Query 483 TLIDGYCGAKRIDDGMEELHMETETGLVADTTTYNTLIHGFYLVGDNLAAALDLLQEMISS 542
TLI GYC A +DDG+EL EM G+VA+ TY TLI GF VG++N +LD+ QEMISS
Sbjct 303 TLITGYCKAGMVDDGLLFCCEMGRGIVANAITYITLIRGFRKVGNNINGSLDIFQEMISS 362

Query 543 GLCPDIVTCDTLLDGLCDNGKLDKDALEMFKVMQKS 577
G+ PD +T +L GL +LK AL M + +Q S
Sbjct 363 GVPDTTITIRNMLTGLWSKEELKRALAMLEELQMS 397
  
```

Score = 216 bits (551), Expect = 8e-54  
 Identities = 120/392 (30%), Positives = 214/392 (54%), Gaps = 13/392 (3%)

```

Query 160 PSVVDFCKLMGVVVRMERPDVLISLYQMKMERQIRCDIYSFNILIKFCSCSKLPALST 219
P+VV F LM + R R ++L +M ++ + ++ ++ C AL+
Sbjct 4 PNVVTFPTLMMNGLCREGRVVEAVALDRMVEDGLQPNQITYGTIVDGMCKMGDTVSALNL 63

Query 220 FGKIKLG-LHPDVVFTTLLHGLCVEDRVSEALDFHQMFEETTCRPNVVTFTTLMNGLC 278
K+ +L + PDVV ++ ++ GL + R ++A + F +M + P++VT++ ++NG C
Sbjct 64 LRKMEELSHIKPDVVYISAIDGLWKDGRHTDAQNLFIEMQDKGIFPDIVTYSCHINGFC 123
  
```



## Group 5

```

Query 279 REGRIVEAVALDRMEDGLQPTQITYGTIVDGMCKKGDVTSALNLLRKMEEVSHIIPNV 338
          G+ EA LL M+ + P +T+ +++ + K+GD SA +LL+M S + PNV
Sbjct 124 SSGKWSEARLLQEMLVKRIKISPDVVTFSGLINALVKEGDLNSAQDLLQEMIS-SGVCPCNV 182

Query 339 VIYSAIIDSLCKDGRHSDAQNLFTEMQE-----KGIFPDLFYNSMIVGFCSSG 387
          V + ++D LC G+ DA +F MQ+ G+ PD+ TYN +I G + G
Sbjct 183 VTCNTLLDGLCDRGKLDKDALEMFKAMQKSMMDIDATHAFNGVEPDVQTYNIIISGLINEG 242

Query 388 RWSDAEQLLQEMLERKISPDVVTYNALINAFVKEGKFFEAELYDEMLPRGIIPNTITYS 447
          ++ +AE+L +EM R I PD VTY+++IN K+ + EA +++D M + PN +T++
Sbjct 243 KFLAEELYEEMPHRGIVPDTVTYSSMINGLCKQSRLEATQMFDSMGSKSFSPNIVTFN 302

Query 448 SMIDGFCQKQNRDLAAEHMFYLMATKGCSPNLITFNTLIDGYCGAKRIDDMELLHEMTET 507
          ++I G+CK +D +F M +G N IT+ TLI G+ I+ +++ EM +
Sbjct 303 TLTITGYCKAGMVDGDLGLFCFEMGRRGIVANAITYITLIRGFRKVGNGSLDIFQEMISS 362

Query 508 GLVADTTTYNTLIHGFYLVGLNAAALDLLQEM 539
          G+ DT T ++ G + +L AL +L+E+
Sbjct 363 GVPDTTIRNMLTGLWSKEELKRALAMLEEL 394
    
```

Score = 193 bits (491), Expect = 8e-47

Identities = 109/371 (29%), Positives = 193/371 (52%), Gaps = 11/371 (2%)

```

Query 145 DAIDLFSDMLRSRPLSPVDFCKLMGVVVRMERPDLVISLYQKMER-KQIRCDIYSFNIL 203
          +A+ L M+ P+ + + ++ +M ++L +KME I+ D+ ++ +
Sbjct 24 EAVALDRMVEDGLQPNQITYGTIVDGMCKMGDTVSALNLLRKMEELSHIKPDVVYISAI 83

Query 204 IKCFCSCKSLPFALSTFGKITKLGLHPDVVTFITLLHGLCVEDRVSEALDFHQMFFETTC 263
          I + A + F ++ G+ PD+VT++ +++G C + SEA +M
Sbjct 84 IDGLWKDGRHTDAQNLFIEMQDKGIFPDIVTYSKCMINGFCSSGKWSAQRLLEQMLVVRKI 143

Query 264 RPNVVTFTTLNMGLCREGRIVEAVALDRMEDGLQPTQITYGTIVDGMCKKGDVTSALN 323
          P+VVTF+ L-N L +EG + A LL M+ G+ P +T T++DG+C +G AL
Sbjct 144 SPDVVTFSGLINALVKEGDLNSAQDLLQEMISSGVCPCNVVTCNTLLDGLCDRGKLDKDALE 203

Query 324 LLRKME-----EVSH----IIPNVVIYSAIIDSLCKDGRHSDAQNLFTEMQEKGIFPD 373
          + + M+ + +H + P+V Y+ +I L +G+ +A+ L+ EM +GI PD
Sbjct 204 MFKAMQKSMMDIDATHAFNGVEPDVQTYNIIISGLINEGKFLAEELYEEMPHRGIVPDT 263

Query 374 FTYNSMIVGFCSSGRWSDAEQLLQEMLERKISPDVVTYNALINAFVKEGKFFEAELYDE 433
          TY+SMI G C R +A Q+ M + SP++VT+N LI + K G + EL+ E
Sbjct 264 VTYSSMINGLCKQSRLEATQMFDSMGSKSFSPNIVTFNTLITGYCKAGMVDGDLGLFCFCE 323

Query 434 MLPRGIIPNTITYSSMIDGFCQKQNRDLAAEHMFYLMATKGCSPNLITFNTLIDGYCGAKR 493
          M RGI+ N ITY ++I GF K ++ + +F M + G P+ IT ++ G +
Sbjct 324 MGRRGIVANAITYITLIRGFRKVGNGSLDIFQEMISSGVYPTDITIRNMLTGLWSKEE 383

Query 494 IDDMELLHEM 504
          + + +L E+
Sbjct 384 LKRALAMLEEL 394
    
```



## Group 5

- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 7 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 8 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 9 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 10 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 11 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 12 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 13 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 14 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 15 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 16 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 17 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found

## Group 5

- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 18 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 19 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 20 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 21 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 22 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 23 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 24 from Brown provisional No. 3 (60/308,736)**

Score = 1180 bits (3053), Expect = 0.0

Identities = 595/685 (86%), Positives = 629/685 (91%), Gaps = 6/685 (0%)

Query	84	MLARVCGFKCSSPAESAAFLCTRSIRDTLAKAS--GESCEAGFGGESLKLQSGFHEIK	141
Sbjct	1	MLARVC F+ SSS + SAAR FCT SIR LA+ S GES EAGF GESLKL+SG +EIK	
Query	142	GLEDAIDLFSDMLRSRPLPSVVDFFCKLMGVVVRMERPDVLVISLYQKMERKQIRCDIYSFN	201
Sbjct	61	GLEDAIDLFSDMLRSRPLPSV+DF KLMG VVRMERPDVLVISLYQKMERKQIRCDIYSF	
Query	202	ILIKCFCSCKLPFALSTFGKITKLGLHPDVVTFITLLHGLCEDRVSEALDFFHQMFET	261
Sbjct	121	ILIKCFCSCKLPFALSTFGK+TKLGLHPDVVTFITLLHGLC++ RVSEALD FHQ+	
Query	262	TCRPNVVTFITLLMNGLCREGRIVEAVALDRMEDGLQPTQITYGTIVDGMCKKGDVTVA	321
Sbjct	178	CRP-V+TFITLLMNGLCREGR+VEAVALDRM+E+GLQP QITYGT VDGCK GDVTVA	
		-CRPDLVTFITLLMNGLCREGRVVEAVALDRMVENGLQPDQITYGTIVDGMCKKGDVTVA	236

## Group 5

Query	322	LNLLRKMEEVSHIIPNVVIYSAIDSLCKDGRHSDAQNLFTEMQEKGIFPDFTYNSMIV	381
Sbjct	237	LNLLRKMEE+SHI PNVVIYSAID LCKDGRHSD+ NLF EMQ+KGIFP++ TYN MI	296
Query	382	GFCSSGRWSDAEQLLQOEMLERKISPVDVVTYNALINAFVKEGKFFEAELYDEMLPRGIIP	441
Sbjct	297	GFCISGRWSAAQRLQOEMLERKISPVDVVTYNALINAFVKEGKFFEAELYDEMLPRGIIP	356
Query	442	NTITYSSMIDGFCKQNRDLDAEHEMFYLMATKGCSNLTITNTLIDGYCGAKRIDDMGELL	501
Sbjct	357	NTITY+SMIDGFCKQ+RLDAE MFYLMATKGCSNLTITNTLIDGYCGAKRIDDMGELL	416
Query	502	HEMTETGLVADTTTYNTLIHGFIYLVGDLNAAEDLLQOEMISSGLCPDIVTCPTLLDGLCDN	561
Sbjct	417	HEMPRRGLVANTVTYNTLIHGFIYLVGDLNAAEDLLSQQMISSGVCPDIVTCNTLLDGLCDN	476
Query	562	GKLKDALEMPKVMQKSKKDLDAHPFNGVEPDVQTYNIIISGLINEGKFLAEELYEEMP	621
Sbjct	477	GKLKDALEMPK MQSK DLDASHPFNGVEPDV TYNII GLINEGKFLAEELYEEMP	536
Query	622	HRGIVPDTITYSSMIDGLCKQSRLEATQMFDSMGSKSFSPNVVFTTLINGYCKAGRVD	681
Sbjct	537	HRGIVPDTITYSSMIDGLCKQSRLEATQMF SMGSKSFSPNVVFT TLINGYCKAGRVD	596
Query	682	DGLELFCCEMGRRGIVANAITYITLICGFRKVGNGINGALDIFQOEMISSGVYPTITIRNML	741
Sbjct	597	DGLELFCCEMGRRGIVA+AI YITLI GFRKVGNGINGALDIFQOEMISSGVYPTITIRNML	656
Query	742	TGLWSKEELKRAVAMLEQLQMSMVY 766	
Sbjct	657	TG WSKEEL+RAVAMLE LQMS+ Y	
		TGFWSKEELERAVAMLEDLQMSVGY 681	

- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 25 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 26 from Brown provisional No. 3 (60/308,736)**

Score = 1624 bits (4206), Expect = 0.0

Identities = 804/804 (100%), Positives = 804/804 (100%), Gaps = 0/804 (0%)

Query	1	MEAPNYPIFFGLNLGVPLEGGRSGTYSGFGSSLFGRIFGVKDFSPIRFLNYGSGSVRI	60
Sbjct	1	MEAPNYPIFFGLNLGVPLEGGRSGTYSGFGSSLFGRIFGVKDFSPIRFLNYGSGSVRI	60
Query	61	LADSSRVFFDRRRRTKFRNNKNKMLARVCGFKCSSSPAESAARLFTCSIRDTLAKASGE	120
Sbjct	61	LADSSRVFFDRRRRTKFRNNKNKMLARVCGFKCSSSPAESAARLFTCSIRDTLAKASGE	120

## Group 5

Query	121	SCEAGFGGESLKLQSGFHEIKGLEDAIDLFSMDLSRSLPSVVDCKLMGVVVRMERPD	180
		SCEAGFGGESLKLQSGFHEIKGLEDAIDLFSMDLSRSLPSVVDCKLMGVVVRMERPD	
Sbjct	121	SCEAGFGGESLKLQSGFHEIKGLEDAIDLFSMDLSRSLPSVVDCKLMGVVVRMERPD	180
Query	181	VISLYQKMERKQIRCDIYSPNLIKCFCSCKLPALSTFGKITKLGLHPDVVFTTLLH	240
		VISLYQKMERKQIRCDIYSPNLIKCFCSCKLPALSTFGKITKLGLHPDVVFTTLLH	
Sbjct	181	VISLYQKMERKQIRCDIYSPNLIKCFCSCKLPALSTFGKITKLGLHPDVVFTTLLH	240
Query	241	GLCVEDRVSEALDFFHQMFETTCRPNVVTFTTLMNGLCREGRIVEAVALDRMMEDGLQ	300
		GLCVEDRVSEALDFFHQMFETTCRPNVVTFTTLMNGLCREGRIVEAVALDRMMEDGLQ	
Sbjct	241	GLCVEDRVSEALDFFHQMFETTCRPNVVTFTTLMNGLCREGRIVEAVALDRMMEDGLQ	300
Query	301	TQITYGTIVDGMCKKGDVTSALNLLRKMEEVSHIIPNVVIYSAIDSLCKDGRHSDAQN	360
		TQITYGTIVDGMCKKGDVTSALNLLRKMEEVSHIIPNVVIYSAIDSLCKDGRHSDAQN	
Sbjct	301	TQITYGTIVDGMCKKGDVTSALNLLRKMEEVSHIIPNVVIYSAIDSLCKDGRHSDAQN	360
Query	361	FTEMQEKGIFFDLFTYNSMIVGFCSSGRWSDAEQLLOEMLERKISPDDVTYNALINAFVK	420
		FTEMQEKGIFFDLFTYNSMIVGFCSSGRWSDAEQLLOEMLERKISPDDVTYNALINAFVK	
Sbjct	361	FTEMQEKGIFFDLFTYNSMIVGFCSSGRWSDAEQLLOEMLERKISPDDVTYNALINAFVK	420
Query	421	EGKFPEAEELYDEMLPRGIIIPNTITYSSMIDGFCQKQNRDLAAEHMFYLMATKGCSPN	480
		EGKFPEAEELYDEMLPRGIIIPNTITYSSMIDGFCQKQNRDLAAEHMFYLMATKGCSPN	
Sbjct	421	EGKFPEAEELYDEMLPRGIIIPNTITYSSMIDGFCQKQNRDLAAEHMFYLMATKGCSPN	480
Query	481	FNTLDIGYCGAKRIDGMEMLHEMTETGLVADTTTYNTLHGFYLVGDLNAALDLLQEMI	540
		FNTLDIGYCGAKRIDGMEMLHEMTETGLVADTTTYNTLHGFYLVGDLNAALDLLQEMI	
Sbjct	481	FNTLDIGYCGAKRIDGMEMLHEMTETGLVADTTTYNTLHGFYLVGDLNAALDLLQEMI	540
Query	541	SSGLCPDIVTCDTLLDGLCDNGKLDKDALEMFVKVMQSKKDLDAHPFNFGVEPVDQTYN	600
		SSGLCPDIVTCDTLLDGLCDNGKLDKDALEMFVKVMQSKKDLDAHPFNFGVEPVDQTYN	
Sbjct	541	SSGLCPDIVTCDTLLDGLCDNGKLDKDALEMFVKVMQSKKDLDAHPFNFGVEPVDQTYN	600
Query	601	ISGLINEGKFLAEELYEEMPHRGIVPDTITYSSMIDGLCKQSRLEATQMFDSMGSKSF	660
		ISGLINEGKFLAEELYEEMPHRGIVPDTITYSSMIDGLCKQSRLEATQMFDSMGSKSF	
Sbjct	601	ISGLINEGKFLAEELYEEMPHRGIVPDTITYSSMIDGLCKQSRLEATQMFDSMGSKSF	660
Query	661	SPNVVFTTTLINGYCKAGRVDDGLELFCMGRRGIVANAITIYITLICGFRKVGNGINGALD	720
		SPNVVFTTTLINGYCKAGRVDDGLELFCMGRRGIVANAITIYITLICGFRKVGNGINGALD	
Sbjct	661	SPNVVFTTTLINGYCKAGRVDDGLELFCMGRRGIVANAITIYITLICGFRKVGNGINGALD	720
Query	721	IFQEMISSGVYPTITIRNMLTGLWSKEELKRAVAMLEKLQMSMVYYWSELKRHTFQKIS	780
		IFQEMISSGVYPTITIRNMLTGLWSKEELKRAVAMLEKLQMSMVYYWSELKRHTFQKIS	
Sbjct	721	IFQEMISSGVYPTITIRNMLTGLWSKEELKRAVAMLEKLQMSMVYYWSELKRHTFQKIS	780
Query	781	GVKRCLGVCPCFCSCHHGYYQARSS 804	
		GVKRCLGVCPCFCSCHHGYYQARSS	
Sbjct	781	GVKRCLGVCPCFCSCHHGYYQARSS 804	

- SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 27 from Brown provisional No. 3 (60/308,736)

## Group 5

Score = 975 bits (2521), Expect = 0.0

Identities = 511/690 (74%), Positives = 569/690 (82%), Gaps = 48/690 (6%)

Query	84	MLARVCGFKCSSPAESARLFCTRSIRDTLAKASGESCEAGFGGESLKLQSGFHEIKGL	143
		MLARV SSSPA SAARLFCTRSIR LAK S + E+GFGGESLKL+SGFHEIKGL	
Sbjct	1	MLARVYRSGSSSPAVSAARLFCTRSIRHALAKKSRDG-ESGFGGESLKLRSQGFHEIKGL	59
Query	144	EDAIDLFDMLRSRPLPSVDFCKLMGVVVRMERPDVLVISLYQKMERQIRCDIYSFNIL	203
		EDAIDLFDMLRSRPLPSVDFCKLMGVVVRMERPDVLVISLYQKMERQIRCDIYSFNIL	
Sbjct	60	EDAIDLFDGMVRSRPLPSVIDFCKLMGVVVRMRGLDVVISLHRKMEMRRVPCNAYSFTIL	119
Query	204	IKCFCSCKLPPALSTFGKITKLGLHPDVVTFITLLHGLCVDREVSEALDFHQMFFETTC	263
		+KCFCSCKLPPALSTFGKITKLGL FH	
Sbjct	120	MKCFCSCKLPPALSTFGKITKLGL-----FH-----	145
Query	264	RPNVVFITLLMNLGCREGRIVEAVALDRMMEDGLQPTQITYGTIVDGMCKKGDVTSALN	323
		P VVTF+TL++GLC E RI EA+ L +M + P +T+ T++G+C++G V A+	
Sbjct	146	-PTVVFITLLHGLCVDREVSEALDFHQMCK---PNVVFITLLMNLGCREGRIVEAVAL	200
Query	324	LLRKMEEVSHIIPNVVVISAIIDSLCKDGRHSDAQNLFTEMQEGK-IFPDLFITY-----	377
		LL +M E + PN + Y I+D +CK G A NL +M+E I P++ +	
Sbjct	201	LLDRMLE-DGLQPNQITYGTIVDGMCKKGDVTSALNLLRKMEEVSHIIPNVVVIPLERRT	259
Query	378	SMIVGFCSSGRWSDAEQLQEMLERK-ISPDPVVTYNALINAFVKEGKFFEAEELYDEMPL	436
		M I GFCSSGRWS+A-QLLQEMLERK ISPDPVVTYNALINAFVKEGKFFEAEELYDEMPL	
Sbjct	260	CMINGFCSSGRWSEAQQLQEMLERKKISPDPVVTYNALINAFVKEGKFFEAEELYDEMPL	319
Query	437	RGIIPNTITYSSMIDGFCQKQNRDLAAEHMFYLMATKGCSPNLITFNTLIDGYCGAKRID	496
		RGIIP+TITYSSMIDGFCQKQNRDLAAEHMFYLMATKGCS++ITFNTLI GYC AKR+DD	
Sbjct	320	RGIIPNTITYSSMIDGFCQKQNRDLAAEHMFYLMATKGCSPIITFNTLIAGYCRAKRVDD	379
Query	497	GMEILLHEMTETGLVADTTTYNTLIHGFLYVGLDNLAAQLQEMISSGLCPDITVCDTLLD	556
		G++LLHEMT GLVA+T TY TLHGF VGLDNLAA DLLQEM+SSG+CP++VTC+TLLD	
Sbjct	380	GIKLLHEMTAGLVANTITYTTTLIHGFCQVGLDNLAAQLQEMVSSGVCPPNVVTCNTLLD	439
Query	557	GLCDNGKLKDALEMFKVMQSKKDLASHPFNGVEPDVQTYNIIISGLINEGKFLEAEEL	616
		GLCDNGKLKDALEMFK MQSK D+DASHPFNGVEPDVQTYNIIISGLINEGKFLEAEEL	
Sbjct	440	GLCDNGKLKDALEMFKAMQSKMDIDASHPFNGVEPDVQTYNIIISGLINEGKFLEAEEL	499
Query	617	YEEMPHRGIVPDTITYSSMIDGLCKQSRLEDEATQMFDSMGSKSFSFNVVTFITLINGYCK	676
		YEEMPHRGIVPDTITY+S+I GLCKQSRLEDEATQMFDSMGSKSFSFNVVTFITLINGYCK	
Sbjct	500	YEEMPHRGIVPDTITYNSVIGLCKQSRLEDEATQMFDSMGSKSFSFNVVTFITLINGYCK	559
Query	677	AGRVDDGLELFCMGRRGIVANAIITYITLICGFRKVGNGINGALDIFQEMISSGVYPDIT	736
		AGRVDDGLELFCMGRRGIVANAIITYITLI GERKVGNGINGALDIFQEM++SGVYPDIT	
Sbjct	560	AGRVDDGLELFCMGRRGIVANAIITYITLIHGFRKVGNGINGALDIFQEMASGVYPDIT	619
Query	737	IRNMLTGLWSKEELKRAVAMLEKLQMSMVY 766	
		IRNMLTGLWSKEELKRAVAMLE KLMS+ Y	
Sbjct	620	IRNMLTGLWSKEELKRAVAMLEDLQMSVG 649	

## Group 5

- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 28 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 29 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 30 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 31 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 32 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 33 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 34 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 35 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 36 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 37 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 38 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found



## Group 5

- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 39 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 40 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 41 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 42 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 43 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 1 from Brown provisional No. 1 (60/305,026)**

Score = 521 bits (1341), Expect = 2e-145

Identities = 261/395 (66%), Positives = 311/395 (78%), Gaps = 1/395 (0%)

```

Query 288 PDLETYNSMIVGFCSSGRWSDAEQLLEMLERKISPVDVVTYNALINAFVKEGKFFAEEL 347
P++ T+ +++ G C GR +A LL M+E + P+ +TY +++ K G A L
Sbjct 4 PNVVTFITLMNGLCREGRVVEAVALDRMVDGLQPNQITYGTIVDGCMKMGDTVSALNL 63

Query 348 YDEMLPRGII-PNTITYSSMIDGFCQNRDLAAEHMFYLMATKGCSPNLITFNTLIDGYC 406
+M I P+ + YS++IDG K R A+++F M KG P+++T++ +I+G+C
Sbjct 64 LRKMEELSHIKPDVVIYSAIDGLWKDGRHTDAQNLFIEMQDKGIFPDIVTSCMINGFC 123

Query 407 GAKRIDDMELLHEMTETGLVADTTTYNTLHGFYLVGDLNAAALLQEMISSGLCPDIV 466
+ + + LL EM + D T++ LI+ GDLN+A DLLQEMISSG+CP++V
Sbjct 124 SSGKWSEAQRLLEMLVRKISPVDVVTFSGLINALVKEGDLNSAQDLLQEMISSGVCNVV 183

Query 467 TCDTLDDGLCDNGKLDKDALEMFVKMQSKKDLDAHPFNGVEPDVQTYNIIISGLINEGK 526
TC+TLDDGLCD GKLDKDALEMFK MQKS D+DA+H FNGVEPDVQTYNIIISGLINEGK
Sbjct 184 TCNTLLDGLCDRGKLDKDALEMFKAMQSKMMDIDATHAFNGVEPDVQTYNIIISGLINEGK 243

Query 527 FLEAEELYEEMPHRGIVPDTITYSSMIDGLCKQSRLEATQMFDMSGKSFSPNVVTFIT 586
FLEAEELYEEMPHRGIVPDT+TYSSMI+GLCKQSRLEATQMFDMSGKSFSPN+VTF T
Sbjct 244 FLEAEELYEEMPHRGIVPDTITYSSMIDGLCKQSRLEATQMFDMSGKSFSPNIVTFNT 303
  
```

## Group 5

Query 587 LINGYCKAGRVDGGLFCEMGRRGIVANAITYITLICGFRKVGNGINGALDIFOEMISSG 646  
 LI GYCKAG VDDGGLFCEMGRRGIVANAITYITLI GFRKVGNGING+LDIFOEMISSG  
 Sbjct 304 LITGYCKAGMVDGGLFCEMGRRGIVANAITYITLIRGFRKVGNGINGSLDIFOEMISSG 363  
 Query 647 VYPDTITIRNMLTGLWSKEELKRAVAMLEKLQMSM 681  
 VYPDTITIRNMLTGLWSKEELKRA+AMLE+LQMSM  
 Sbjct 364 VYPDTITIRNMLTGLWSKEELKRALAMLEELQMSM 398

Score = 394 bits (1012), Expect = 2e-107  
 Identities = 208/404 (51%), Positives = 265/404 (65%), Gaps = 22/404 (5%)

Query 180 CRPNVVTFTTLMNGLCREGRIVEAVALDRMMEDGLQPTQITYGTIVDGMCKKGDVTSAL 239  
 C+PNVVTFTTLMNGLCREGR+VEAVALDRM+EDGLQP QITYGTIVDGMCK GDVTSAL  
 Sbjct 2 CKPNVVTFTTLMNGLCREGRVEAVALDRMVEDGLQPNQITYGTIVDGMCKMGDVTSA 61  
 Query 240 NLLRKMEEVSHIIPNVVIYSAIDSLCKDGRHSDAQNLFTEMQEKGIFFDLFTYNSMIVG 299  
 NLLRKMEE+SHI P+VVIYSAIID L KDGRH+DAQNLF EMQ+KGIFPD+ TY+ MI G  
 Sbjct 62 NLLRKMEELSHIKPDVVIYSAIDGLWKDGRHTDAQNLFEMQDKGIFFDIVTYS 121  
 Query 300 FCSSGRWSDAEQLLQEMLERKISPDVVTYNALINAFVKEGKFFAEELYDEMLPRGIIPN 359  
 FCSSG+WS+A+LLQEML RKISPDVVT++ LINA VKEG A++L EM+ G+ PN  
 Sbjct 122 FCSSGKWSAEQRLQEMLVRKISPDVVTFSGLINALVKEGDLNSAQDLLQEMISSGVCPN 181  
 Query 360 TITYSSMIDGFCQNRDLAAEHMFYLM-----ATKGCSPNLITFNTLIDGYCGA 408  
 +T +++++DG C + +L A MF M A G P++ T+N LI G  
 Sbjct 182 VVTCNTLLDGLCDRGKLDKDALEMFAMQKSMMDIDATHAFNGVEPDVQTYNIIISGLINE 241  
 Query 409 KRIDDGMELLHEMTETGLVADTTTYNTLIHGFYLVGDLNAAALLQEMISSGLCPDIVTC 468  
 + + EL EM G+V DT TY+++I+G L+A + M S P+IVT  
 Sbjct 242 GKFLAEAEELYEEMPHRGIVPDTVITYSSMINGLCKQSRLEATQMFDSMGSKSFNIVTF 301  
 Query 469 DTLLDGLCDNGKLDKDALEMFVKMQKSKKDLASHFPNGVEPDVQTYNIIISGLINEGKFL 528  
 +TL+ G C G + D LE+F M + G+ + TY LI G G  
 Sbjct 302 NTLITGYCKAGMVDGGLFCEMGR-----RGIVANAITYITLIRGFRKVGNGIN 350  
 Query 529 EAEELYEEMPHRGIVPDTITYSSMIDGLCKQSRLEATQMFDSM 572  
 + ++++EM G+ PDTIT +M+ GL + L A M + +  
 Sbjct 351 GSLDIFQEMISSGVYPDTITIRNMLTGLWSKEELKRALAMLEEL 394

Score = 300 bits (767), Expect = 6e-79  
 Identities = 166/395 (42%), Positives = 229/395 (57%), Gaps = 48/395 (12%)

Query 147 PDVVTFTTLLHGLCVDREVSEALDFHQMFEETCRPNVVTFTTLMNGLCREGRIVEAVAL 206  
 P+VVTFTTLL+GLC E RV EA+ +M E +PN +T+ T+++G+C+ G V A+ L  
 Sbjct 4 PNVVFTTLLMNGLCREGRVVEAVALDRMVEDGLQPNQITYGTIVDGMCKMGDVTSA 63  
 Query 207 LDRMME-DGLQPTQITYGTIVDGMCKKGDVTSALNLLRKMEEVSHIIPNVVIYSAIDSL 265  
 L +M E ++P + Y I+DG+ K G A NL +M++ I P++V YS +I+  
 Sbjct 64 LRKMEELSHIKPDVVIYSAIDGLWKDGRHTDAQNLFEMQD-KGIFPDIVTYS 122

## Group 5

```

Query 266 CKDGRHSDAQNLFTEMQEKGIFPDFTYNSMIVGFCSSGRWSDAEQLLOEMLE----- 318
          C  G+ S+AQ L  EM  + I PD+ T++ +I      G  + A+ LLQEM+
Sbjct 123 CSSGKWSEAQRLLQEMLVKISPDVVTFSGLINALVKEGDLNSAQDLLQEMISSGVCPNV 182

Query 319 -----RKISPDVVITYNALINAFVKEG 339
          + PDV TYN Li+ + EG
Sbjct 183 VTCNTLLDGLCDRGKLDKDALEMFKAMQKSMMDIDATHAFNGVEPDVQTYNIIISGLINEG 242

Query 340 KFFEAEELYDEMLPRGIIPNTITYSSMIDGFCQNRLDAAEHMFYLMATKGCSPNLITFN 399
          KF EAEELY+EM  RGI+P+T+TYSSMI+G CKQ+RLD A  MF  M +K  SPN++TFN
Sbjct 243 KFLEAEELYEEMPHRGIVPDTVTYSSMINGLCKQSRLEATQMFDSMGSKSFSPNIVTFN 302

Query 400 TLIDGYCGAKRIDDMELHMETETGLVADTTTYNTLIHGIFYLVGDLNAAALDLLQEMISS 459
          TLI GYC A +DDG+EL  EM  G+VA+  TY TLI GF  VG++N +LD+ QEMISS
Sbjct 303 TLTITGYCKAGMVDGLELFCMGRRGIVANAITYITLIRGFRKVGNGSLDIFQEMISS 362

Query 460 GLCPDIVTCDTLLDGLCDNGKLDKDALEMFKVMQKS 494
          G+ PD +T  +L GL  +LK AL M + +Q S
Sbjct 363 GVPYPTITIRNMLTGLWSKEELKRALAMLEELQMS 397
    
```

Score = 216 bits (551), Expect = 7e-54

Identities = 120/392 (30%), Positives = 214/392 (54%), Gaps = 13/392 (3%)

```

Query 77 PSVVDPFCKLMGVVVRMERPDVLVISLYQKMERKQIRCDIYSFNILIKCFCSCSKLPFALST 136
          P+VV F  LM  + R R  ++L +M  ++ + ++ ++  C  AL+
Sbjct 4  PNVVTFITLMLNGLCREGRVVEAVALDRMVEDGLQPNQITYGTIVDGMCKMGDTVSALNL 63

Query 137 FGKITKLGL-LHPDVTFTTLLHGLCVEDRVSEALDFHQMFEETTCRPNVVTFTTLMNGLC 195
          K+ +L  + PDVV ++ ++ GL  + R ++A + F +M +  P++VT++ ++NG C
Sbjct 64 LRKMEELSHIKPDVVVYSAIDGLWKDGRHTDAQNLFIEQMCKGIFPDIVTYSKMGNGFC 123

Query 196 REGRIEAVALLDRMMDGLQPTQITYGTIVDGMCKKGDTSVALNLLRKMEEVSHIIPNV 255
          G+ EA LL M+  + P  +T+  +++ + K+GD SA +LL+M  S + PNV
Sbjct 124 SSGKWSEAQRLLQEMLVKISPDVVTFSGLINALVKEGDLNSAQDLLQEMIS-SGVCPNV 182

Query 256 VIYSAIDSLCKDGRHSDAQNLFTEMQE-----KGIFPDFTYNSMIVGFCSSG 304
          V  + ++D LC  G+  DA  +F MQ+      G+ PD+ TYN +I G  + G
Sbjct 183 VTCNTLLDGLCDRGKLDKDALEMFKAMQKSMMDIDATHAFNGVEPDVQTYNIIISGLINEG 242

Query 305 RWSDAEQLLOEMLERKISPDVVITYNALINAFVKEGKFFEAEELYDEMLPRGIIPNTITYS 364
          ++ +AE+L +EM  R I PD VTY++IN  K+ + EA +++D M  +  PN +T++
Sbjct 243 KFLEAEELYEEMPHRGIVPDTVTYSSMINGLCKQSRLEATQMFDSMGSKSFSPNIVTFN 302

Query 365 SMIDGFCQNRLDAAEHMFYLMATKGCSPNLITFNTLIDGYCGAKRIDDMELHMETET 424
          ++I G+CK  +D  +F M  +G  N IT+ TLI G+  I+  +++ EM  +
Sbjct 303 TLTITGYCKAGMVDGLELFCMGRRGIVANAITYITLIRGFRKVGNGSLDIFQEMISS 362

Query 425 GLVADTTTYNTLIHGIFYLVGDLNAAALDLLQEM 456
          G+ DT T  ++ G +  +L AL +L+E+
Sbjct 363 GVPYPTITIRNMLTGLWSKEELKRALAMLEEL 394
    
```

## Group 5

Score = 193 bits (49%), Expect = 6e-47  
 Identities = 109/371 (29%), Positives = 193/371 (52%), Gaps = 11/371 (2%)

```

Query 62 DAIDLFSDMLRSRPLPSVVDFCKLMGVVVRMERPDLVISLYQKMER-KQIRCDIYSFNIL 120
      +A+ L M+ P+ + + ++ + +M ++L +KME I+ D+ ++ +
Sbjct 24 EAVALLDRMVEDGLQPNQITYGTIVDGMCKMGDTVSALNLLRMEELSHIKPDVVIYSAI 83

Query 121 IKCFSCSKLPFALSTFGKITKLGHPDVVTFITLLHGLCVEDRVSEALDFFHQMFETTC 180
      I + A + F ++ G+ PD+VT++ ++G C + SEA +M
Sbjct 84 IDGLWKDGRHTDAQNLFIEMQDKGIFPDIVTYSCHINGFCSSGKWSEARLLQEMLVRKI 143

Query 181 RPNVVTFTTLMNGLCREGRIVEAVALLDRMMEDGLQPTQITYGTIVDGMCKKGDTSALN 240
      P+VVTF+ L+N L +EG + A LL M+ G+ P +T T++DG+C +G AL
Sbjct 144 SPDVVTFSGLINALVKEGDLNSAQDLLQEMISSGVCPNVVTCNTLLDGLCDRGKLDKDALE 203

Query 241 LLRKME-----EVSH---IIPNVVIYSAIDSLCKDGRHSDAQNLFTEMQEKGIFPD 290
      + + M+ + +H + P+V Y+ +I L +G+ +A+ L+ EM +GI PD
Sbjct 204 MPKAMQKSMMDIDATHAFNGVEPDVQTYNIIISGLINEGKFLAEELYEEMPHRGIVPDT 263

Query 291 FTYNSMIVGFCSSGRWSDAEQLLOEMLERKISPVDVVTYNALINAFVKEGKFEEAEELYDE 350
      TY+SMI G C R +A Q+ M + SP++VT+N LI + K G + EL+ E
Sbjct 264 VTYSSMINGLCKQSRLEATQMFDSMGSKSFPNIVTFNTLITGYCKAGMVDDGLELPCE 323

Query 351 MLPRGIIPNTITYSSMIDGFCQNRDLAAEHMFYLMATKGCSFNLTFTNLIDGYCGAKR 410
      M RGI+ N ITY ++I GF K ++ + +F M + G P+ IT ++ G +
Sbjct 324 MGRRGIVANAITYITLIRGFRKVGNGSLDIFQEMISSGVYVPDTITIRNMLTGLWSKEE 383

Query 411 IDGMEELHEM 421
      + + +L E+
Sbjct 384 LKRALAMLEEL 394
  
```

Score = 118 bits (29%), Expect = 3e-24  
 Identities = 78/282 (27%), Positives = 130/282 (46%), Gaps = 12/282 (4%)

```

Query 52 SGFHEIKGLEDAIDLFSDMLRSRPLPSVVDFCKLMGVVVRMERPDLVISLYQKMERKQIR 111
      +GF +A L +ML + P VV F L+ +V+ + L Q+M +
Sbjct 120 NGFCSSGKWSEARLLQEMLVRKISPVDVTFSGLINALVKEGDLNSAQDLLQEMISSGVC 179

Query 112 CDIYSFNILIKCFSCSKLPFALSTFGKITKL-----GLHPDVVTFITLLHGLC 160
      ++ + N L+ C KL AL F + K G+ PDV T+ L+ GL
Sbjct 180 PNVVTCNTLLDGLCDRGKLDKDALEMPKAMQKSMMDIDATHAFNGVEPDVQTYNIIISGLI 239

Query 161 VEDRVSEALDFFHQMFETTCRPNVVTFITLMNGLCREGRIVEAVALLDRMMEDGLQPTQI 220
      E + EA + + +M P+ VT+++++NGLC++ R+ EA + D M P +
Sbjct 240 NEGKFLAEELYEEMPHRGIVPDTVITYSSMINGLCKQSRLEATQMFDSMGSKSFPNIV 299
  
```

## Group 5

Query	221	TYGTIVDGMCKKGDTSALNLLRKMEEVSHIIPNVVIYSALISLCKDGRHSDAQNLFT	280
		T+ T++ G CK G L L +M I+ N + Y +I K G + + ++F E	
Sbjct	300	TFTLTITGYCKAGMVDGGLFCEMGRRG-IVANAITYITLIRGFRKVGNGSLDIFQE	358
Query	281	MQEKGIFPDLTFTYNSMIVGFCSSGRWSDAEQLLQEMLERKIS	322
		M G++PD T +M+ G S A +L+E+ +S	
Sbjct	359	MISSGVYPDTTITRNMLTGLWSKEELKRALAMLEELQMSMVS	400

- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 2 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 3 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 4 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 5 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 6 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 7 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 8 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 9 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 10 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found

## Group 5

- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 11 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 12 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 13 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 14 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 15 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 16 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 17 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 18 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 19 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 20 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 21 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found

## Group 5

- SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 22 from Brown provisional No. 1 (60/305,026)

Score = 1179 bits (3049), Expect = 0.0

Identities = 594/683 (86%), Positives = 628/683 (91%), Gaps = 6/683 (0%)

Query	1	MLARVCGFKCSSPAESARLFCSTRSIRDTLAKAS--GESCEAGFGGESLKLQSGFHEIK	58
Sbjct	1	MLARVC P+ SSS + SAAR FCT SIR LA+ S GES EAGF GESLKL+SG +EIK	60
Query	59	GLEDAIDLFSDMLRSRPLSPVDFCKLMGVVVRMERPDVLISLYQKMERKQIRCDIYSFN	118
Sbjct	61	GLEDAIDLFSDMLRSRPLSPV+DF KLMG VVRMERPDVLISLYQKMERKQIRCDIYSF	120
Query	119	ILIKCFCSCSKLPFALSTFGKITKLGLHPDVVFTFTLLHGLCEDRVSEALDFFHQMFET	178
Sbjct	121	ILIKCFCSCSKLPFALSTFGK+TKLGLHPDVVFTFTLLHGLC++ RVSEALD FHQ+	177
Query	179	TCRPNVVFTFTLLMNGLCREGRIVEAVALDRMMDGLQPTQITYGTIVDMCKKGDVTSA	238
Sbjct	178	CRP+V+FTFTLLMNGLCREGR+VEAVALDRM+E+GLQP QITYGT VDMCK GDVTSA	236
Query	239	LNLLRKMEEVSHIIPNVVIYSAIIDSCKDGRHSDAQNLTTEMQEKGFPPDLFTYNSMIV	298
Sbjct	237	LNLLRKMEE+SHI PNVVIYSAIID LCKDGRHSD+ NLF EMQ+KGFFP++ TYN MI	296
Query	299	GFCSSGRWSDAEQLLQEMLERKISPVDVTYNALINAFVKEGKFFEAELYDEMLPRGIIP	358
Sbjct	297	GFC SGRWS A++LQEMLERKISP+VVTYNALINAFVKEGKFFEA ELYDEMLPRGIIP	356
Query	359	NTITYSSMIDGFCQNRDLAAEHMFYLMATKGCSPNLTFTNTLIDGYCGAKRIDDGMELL	418
Sbjct	357	NTITY+SMIDGFCQ+RLDAE MFYLMATKGCSP++ TF TLIDGYCGAKRIDDGMELL	416
Query	419	HEMTETGLVADTTTYNTLIHGFLVGLDNLAAALDLQEMISSGLCPDIVTC+TLLDGLCDN	478
Sbjct	417	HEM GLVA+T TYNTLIHG FLVGLDNLAAALDL Q+MISSG+CPDIVTC+TLLDGLCDN	476
Query	479	GKLKDALEMFQMVKQSKKDLASHPFNGVEPDVQTYNIIISGLINEGKFLAEELYEEMP	538
Sbjct	477	GKLKDALEMFK MQKSK DLDASHPFNGVEPDV TYNII GLINEGKFLAEELYEEMP	536
Query	539	HRGIVPDITITYSSMIDGLCKQSRLEATQMFDSMGSKSFSPNVVFTFTTLINGYCKAGRVD	598
Sbjct	537	HRGIVPDITITYSSMIDGLCKQSRLEATQMF SMGSKSFSPNVVTF TLINGYCKAGRVD	596
Query	599	DGLELFCFCEMGRGIVANAITYITLICGFRKVGNGINGALDIFQEMISSGVYDPDITIRNML	658
Sbjct	597	DGLELFCFCEMGRGIVAAIYITLIYGRKVGNGINGALDIFQEMISSGVYDPDITIRNML	656

## Group 5

Query 659 TGLWSKEELKRAVAMLEKLQMSM 681  
 TG WSKEEL+RAVAMLE LQMS+  
 Sbjct 657 TGFWSKEELERAVAMLEDLQMSV 679

- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 23 from Brown provisional No. 1 (60/305,026)**
  - o No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 24 from Brown provisional No. 1 (60/305,026)**

Score = 1368 bits (3541), Expect = 0.0  
 Identities = 681/681 (100%), Positives = 681/681 (100%), Gaps = 0/681 (0%)

Query 1 MLARVCGFKCSSPAESARLFCSTRSIRDTLAKASGESCEAGFGGESLKLQSGFHEIKGL 60  
 MLARVCGFKCSSPAESARLFCSTRSIRDTLAKASGESCEAGFGGESLKLQSGFHEIKGL  
 Sbjct 84 MLARVCGFKCSSPAESARLFCSTRSIRDTLAKASGESCEAGFGGESLKLQSGFHEIKGL 143

Query 61 EDAIDLFSMDLRSRPLPSVVDFFCKLMGVVVRMERPDVLISLYQKMERQIRCDIYSFNIL 120  
 EDAIDLFSMDLRSRPLPSVVDFFCKLMGVVVRMERPDVLISLYQKMERQIRCDIYSFNIL  
 Sbjct 144 EDAIDLFSMDLRSRPLPSVVDFFCKLMGVVVRMERPDVLISLYQKMERQIRCDIYSFNIL 203

Query 121 IKCFCSCKLFFALSTFGKITKLGLHPDVVTFITLLHGLCVDREVSEALDFFHQMFETTC 180  
 IKCFCSCKLFFALSTFGKITKLGLHPDVVTFITLLHGLCVDREVSEALDFFHQMFETTC  
 Sbjct 204 IKCFCSCKLFFALSTFGKITKLGLHPDVVTFITLLHGLCVDREVSEALDFFHQMFETTC 263

Query 181 RPNVVTFITLLMNGLCREGRIVEAVALDRMMEDGLQPTQITYGTIVDGMCKKGDVTSALN 240  
 RPNVVTFITLLMNGLCREGRIVEAVALDRMMEDGLQPTQITYGTIVDGMCKKGDVTSALN  
 Sbjct 264 RPNVVTFITLLMNGLCREGRIVEAVALDRMMEDGLQPTQITYGTIVDGMCKKGDVTSALN 323

Query 241 LLRKMEEVSHIIPNVVIYSAIIDS LCKDGRHSDAQNLFTEMQEKGIFFDLFTYNSMIVGF 300  
 LLRKMEEVSHIIPNVVIYSAIIDS LCKDGRHSDAQNLFTEMQEKGIFFDLFTYNSMIVGF  
 Sbjct 324 LLRKMEEVSHIIPNVVIYSAIIDS LCKDGRHSDAQNLFTEMQEKGIFFDLFTYNSMIVGF 383

Query 301 CSSGRWSDAEQLLQEMLERKISPDVVVTYNALINAFVKEGKFEEAEELYDEMLPRGIIPNT 360  
 CSSGRWSDAEQLLQEMLERKISPDVVVTYNALINAFVKEGKFEEAEELYDEMLPRGIIPNT  
 Sbjct 384 CSSGRWSDAEQLLQEMLERKISPDVVVTYNALINAFVKEGKFEEAEELYDEMLPRGIIPNT 443

Query 361 ITYSSMIDGFCKQNRDLAAEHMFYLMATKGCSPNLITFTNLIDGYCGAKRIDDMELLHE 420  
 ITYSSMIDGFCKQNRDLAAEHMFYLMATKGCSPNLITFTNLIDGYCGAKRIDDMELLHE  
 Sbjct 444 ITYSSMIDGFCKQNRDLAAEHMFYLMATKGCSPNLITFTNLIDGYCGAKRIDDMELLHE 503

Query 421 MTETGLVADTTTNTLIHGFIYLVGDLNAAIDLQEMISSGLCPDIVTCDTLLDGLCDNGK 480  
 MTETGLVADTTTNTLIHGFIYLVGDLNAAIDLQEMISSGLCPDIVTCDTLLDGLCDNGK  
 Sbjct 504 MTETGLVADTTTNTLIHGFIYLVGDLNAAIDLQEMISSGLCPDIVTCDTLLDGLCDNGK 563

Query 481 LKDALEMFVKMQSKKDL DASHFPNGVEPDVQTYNILISGLINEGKFLAEELYEEMPHR 540  
 LKDALEMFVKMQSKKDL DASHFPNGVEPDVQTYNILISGLINEGKFLAEELYEEMPHR  
 Sbjct 564 LKDALEMFVKMQSKKDL DASHFPNGVEPDVQTYNILISGLINEGKFLAEELYEEMPHR 623



## Group 5

Query	541	GIVPDTITYSSMIDGLCKQSRLEATQMFDSMGSKSFSPNVVFTTTLINGYCKAGRVDG	600
		GIVPDTITYSSMIDGLCKQSRLEATQMFDSMGSKSFSPNVVFTTTLINGYCKAGRVDG	
Sbjct	624	GIVPDTITYSSMIDGLCKQSRLEATQMFDSMGSKSFSPNVVFTTTLINGYCKAGRVDG	683
Query	601	LELPCMGRRGIVANAITYITLICGFRKVGNGINGALDIFQEMISSGVYPDTITIRNMLTG	660
		LELPCMGRRGIVANAITYITLICGFRKVGNGINGALDIFQEMISSGVYPDTITIRNMLTG	
Sbjct	684	LELPCMGRRGIVANAITYITLICGFRKVGNGINGALDIFQEMISSGVYPDTITIRNMLTG	743
Query	661	LWSKEELKRAVAMLEKLQMSM	681
		LWSKEELKRAVAMLEKLQMSM	
Sbjct	744	LWSKEELKRAVAMLEKLQMSM	764

- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 25 from Brown provisional No. 1 (60/305,026)**

Score = 974 bits (2517), Expect = 0.0

Identities = 510/688 (74%), Positives = 568/688 (82%), Gaps = 48/688 (6%)

Query	1	MLARVCGKCSSPAESARLFCRTRIRDTLAKASGESCEAGFGGESLKLQSGFHEIKGL	60
		MLARV SSSPA SAARLFCRTRIR LAK S + E+GFGGESLKL+SGFHEIKGL	
Sbjct	1	MLARVYRSGSSSPAVSAARLFCRTRIRHALAKKSRDG-ESGFGGESLKLRSFGFHEIKGL	59
Query	61	EDAIDLFSMDLRSRPLSVVDFCKLMGVVVRMERPDVISLYQKMERKQIRCDIYSFNIL	120
		EDAIDL F DM+RSRPLSPV+DFCKLMGVVVRM R D+VISL++KME +++ C+ YSF IL	
Sbjct	60	EDAIDLFGDMVRSRPLSPVIDFCKLMGVVVRMRDLVDVISLHRKMEMRVRPCNAYSFTIL	119
Query	121	IKCFCSCKLFPALSTFGKITKGLGLHPDVVFTTLLHGLCVEDRVSEALDFFHQMFETTC	180
		+KCFCSCKLFPALSTFGKITKGL FH	
Sbjct	120	MKCFCSCKLFPALSTFGKITKGL-----FH-----	145
Query	181	RPNVVTFTTLNGLCREGRIVEAVALDRMMEDGLQPTQITYGTIVDMCKKGDTVSALN	240
		P VVTF+TL++GLC E RI EA+ L +M + P +T+ T+++G+C++G V A+	
Sbjct	146	-PTVVTFTTLHGLCVEDRISALDLFHQMCK---PNVVTFTTLNGLCREGRVVEAVA	200
Query	241	LLRKMEEVSHIIPNVVIYSAIIDSCKDGRHSDAQNLFTEMQEKQ-IFPDLFITY-----N	294
		LL +M E + PN + Y I+D +CK G A NL +M+E I P++ +	
Sbjct	201	LLDRMLE-DGLQPNQITYGTIVDMCKMGDTVSALNLLRMEEVSHIIPNVVWPLERRT	259
Query	295	SMIVGFCSSGRWSDAEQLQEMLERK-ISPDDVVTYNALINAFVKEGKFEEAEELYDEMPL	353
		MI GFCSSGRWS+A-QLLQEMLERK ISPDDVVTYNALINAFVKEGKFEEAEELYDEMPL	
Sbjct	260	CMINGFCSSGRWSEAEQLQEMLERKKISPDDVVTYNALINAFVKEGKFEEAEELYDEMPL	319
Query	354	RGIIPNTITYSSMIDGFCQNRDLAAEHMFYLMATKGCSPNLTITNTLIDGYCGAKRID	413
		RGIIP+TITYSSMIDGFCQNRDLAAEHMFYLMATKGCSP++ITNTLI GYC AKR+DD	
Sbjct	320	RGIIPSTITYSSMIDGFCQNRDLAAEHMFYLMATKGCSPDITITNTLIAGYCRARVDD	379
Query	414	GMELLHEMTETGLVADTTTYNTLHGFYLVGDLNAAADLLQEMISSGLCPDIVTCDTLLD	473
		G++LLHEMT E GLVA+T TY TLHGF VGDNLAA DLLQEM+SSG+CP++VTC+TLLD	
Sbjct	380	GIKLLHEMT EAGLVANTITYNTLHGFQVGDNLAAADLLQEMVSSGVCPCNVVTCNTLLD	439

## Group 5

Query	474	GLCDNGKLDKDALEMFKVMQSKKDLDDASHPFNGVEPDVQTYNIIISGLINEGKFLAEAEEL	533
		GLCDNGKLDKDALEMFK MQSK D+DASHPFNGVEPDVQTYNIIISGLINEGKFLAEAEEL	
Sbjct	440	GLCDNGKLDKDALEMFKAMQSKMDIDASHPFNGVEPDVQTYNIIISGLINEGKFLAEAEEL	499
Query	534	YEEMPHRGIVPDTITYSSMIDGLCKQSRLEATQMFDSMGSKSFSPNVVTTTTLINGYCK	593
		YEEMPHRGIVPDTITY+S+I GLCKQSRLEATQMFDSMGSKSFSPNVVTTTTLINGYCK	
Sbjct	500	YEEMPHRGIVPDTITYNSVIHGLCKQSRLEATQMFDSMGSKSFSPNVVTTTTLINGYCK	559
Query	594	AGRVDGGLLEFCEMGRRGIVANAITYITLICGFRKVGNGINGALDIFQEMISSGVYPTIT	653
		AGRVDGGLLEFCEMGRRGIVANAITYITLI GFRKVGNGINGALDIFQEM++SGVYPTIT	
Sbjct	560	AGRVDGGLLEFCEMGRRGIVANAITYITLIHGFRKVGNGINGALDIFQEMMASGVYPTIT	619
Query	654	IRNMLTGLWSKEELKRAVAMLEKLQMSM	681
		IRNMLTGLWSKEELKRAVAMLE LQMS+	
Sbjct	620	IRNMLTGLWSKEELKRAVAMLEDLQMSV	647

- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 26 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 27 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 28 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 29 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 30 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 31 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 32 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 33 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found

## Group 5

- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 34 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 35 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 36 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 37 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 38 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 39 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 40 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 41 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against SEQ 4 from Brown provisional No. 2 (60/305,363)**

Score = 1179 bits (3049), Expect = 0.0

Identities = 594/683 (86%), Positives = 628/683 (91%), Gaps = 6/683 (0%)

```

Query 1 MLARVCGFKSSSPAESAARLFCTRSIRDTLAKAS--GESCEAGFGGESLKLQSGFHEIK 58
        MLARVC F+ SSS + SAAR FCT SIR LA+ S GES EAGF GESLKL+SG +EIK
Sbjct 1 MLARVCFRESSSSSVSAARFFCTGSIRHALAEKSRDGEAGFGRGESLKLRSGSYEIK 60

Query 59 GLEDAIDLFSDMLRSRPLPSVVDCKLMGVVVRMERPDLVISLYQKMERKQIRCDIYSFN 118
        GLEDAIDLFSDMLRSRPLPSV+DF KLMG VVRMERPDLVISLYQKMERKQIRCDIYSF
Sbjct 61 GLEDAIDLFSDMLRSRPLPSVIDFNKLMGAVVRMERPDLVISLYQKMERKQIRCDIYSFT 120
  
```

## Group 5

Query	119	ILIKCFCSCSKLPALSTFGKITKLGLHPDVVTFITLLHGLCVEDRVSEALDFFHQMFET	178
Sbjct	121	ILIKCFCSCSKLPALSTFGK+TKLGLHPDVVTFITLLHGLC++ RVSEALD FHQ+	177
Query	179	TCRPNVVVTFITLMNGLCREGRIVEAVALDRMDGLQPTQITYGTIVDGMCKKGTVSA	238
Sbjct	178	CRP+V+FTTLMNGLCREGR+VEAVALDRM+E+GLQP QITYGT VDGCK GTVSA	236
Query	239	LNLLRKMEEVSHIIPNVVIYSAIIDSCKDGRHSDAQNLFTEMQEKGIFPDFTYNSMIV	298
Sbjct	237	LNLLRKMEE+SHIIPNVVIYSAIID LCKDGRHSD+ NLF EMQ+KGIFP++ TYN MI	296
Query	299	GFCSSGRWSDAEQLLQEMLERKISPVDVVTYNALINAFVKEGKFFEAELYDEMLPRGIIP	358
Sbjct	297	GFC SGRWS A++LLQEMLERKISP+VVTYNALINAFVKEGKFFEA ELYDEMLPRGIIP	356
Query	359	NTITYSSMIDGFCQKQNRDLAAEHMFYLMATKGCSPNLTITNTLIDGCGAKRIDDMELL	418
Sbjct	357	NTITY+SMIDGFCQ+RLDAE MFYLMATKGCSP++ TF TLIDGCGAKRIDDMELL	416
Query	419	HEMTETGLVADTTTYNTLHGFYLVGDLNAAALDLQEMISSGLCPDIVTCNTLLDGLCDN	478
Sbjct	417	HEM GLVA-T TYNTLHGF LVGDLNAAALDL Q+MISSG+CPDIVTC+TL DGLCDN	476
Query	479	GKLKDALEMPKVMQKSKKDL DASHFPNGVEPDVQTYNIIISLINEGKFLAEELYEEMP	538
Sbjct	477	GKLKDALEMPK MQSK DLDASHFPNGVEPDV TYNII GLINEGKFLAEELYEEMP	536
Query	539	HRGIVPDITITYSSMIDGLCKQSRLEATQMFDSMGSKSFSPNVVTFITLINGYCKAGRVD	598
Sbjct	537	HRGIVPDITITYSSMIDGLCKQSRLEATQMF SMGSKSFSPNVVTF ITLINGYCKAGRVD	596
Query	599	DGLELFCMGRRGIVANAITVITLICGFRKVGNGINGALDIFQEMISSGVYPTITIRNML	658
Sbjct	597	DGLELFCMGRRGIVA+AI VITLI GFRKVGNGINGALDIFQEMISSGVYPTITIRNML	656
Query	659	TGLWSKEELKRAVAMLEKQMSM 681	
Sbjct	657	TG WSKEEL+RAVAMLE LQMS+ 679	

- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against SEQ 5 from Brown provisional No. 2 (60/305,363)**

Score = 1368 bits (3541), Expect = 0.0  
 Identities = 681/681 (100%), Positives = 681/681 (100%), Gaps = 0/681 (0%)

Query	1	MLARVCGFKCSSPAESAARLFCTRSIRDTLAKASGESCEAGGGESLKLQSGFHEIKGL	60
Sbjct	84	MLARVCGFKCSSPAESAARLFCTRSIRDTLAKASGESCEAGGGESLKLQSGFHEIKGL	143

## Group 5

Query	61	EDAIDLFSMDLRSRPLPSVVDFCCLMGVVVRMERPDVLISLYQKMERKQIRCDIYSFNIL	120
Sbjct	144	EDAIDLFSMDLRSRPLPSVVDFCCLMGVVVRMERPDVLISLYQKMERKQIRCDIYSFNIL	203
Query	121	IKCFCSCSKLPFALSTFGKITKGLGHPDVVTFITLLHGLCVDREVSEALDFFHQMFETTC	180
Sbjct	204	IKCFCSCSKLPFALSTFGKITKGLGHPDVVTFITLLHGLCVDREVSEALDFFHQMFETTC	263
Query	181	RPNVVTFTTLMNGLCREGRIVEAVALDRMMEDGLQPTQITYGTIVDGMCKKGDTVSALN	240
Sbjct	264	RPNVVTFTTLMNGLCREGRIVEAVALDRMMEDGLQPTQITYGTIVDGMCKKGDTVSALN	323
Query	241	LLRKMEEVSHIIPNVVIYSAIIDSLCKDGRHSDAQNLFTEMQEKGIFFDLFTYNSMIVGF	300
Sbjct	324	LLRKMEEVSHIIPNVVIYSAIIDSLCKDGRHSDAQNLFTEMQEKGIFFDLFTYNSMIVGF	383
Query	301	CSSGRWSDAEQLLOEMLERKISPDVVYTINALINAFVKEGKFFAEELYDEMLPRGIIPNT	360
Sbjct	384	CSSGRWSDAEQLLOEMLERKISPDVVYTINALINAFVKEGKFFAEELYDEMLPRGIIPNT	443
Query	361	ITYSSMIDGFCQKQNRDLAAEHMFYLMATKGCSPLNITFTNLIDGYCGAKRIDDMELLHE	420
Sbjct	444	ITYSSMIDGFCQKQNRDLAAEHMFYLMATKGCSPLNITFTNLIDGYCGAKRIDDMELLHE	503
Query	421	MTETGLVADTTTYNTLIHGFIYLVGDLNAAALLQEMISSGLCPDIVTCDTLLDGLCDNGK	480
Sbjct	504	MTETGLVADTTTYNTLIHGFIYLVGDLNAAALLQEMISSGLCPDIVTCDTLLDGLCDNGK	563
Query	481	LKDALEMFKVMQSKKDLASHPFNGVEPDVQTYNILISGLINEGKFLEAEELYEEMPHR	540
Sbjct	564	LKDALEMFKVMQSKKDLASHPFNGVEPDVQTYNILISGLINEGKFLEAEELYEEMPHR	623
Query	541	GIVPDTITYSSMIDGLCKQSRLEATQMFDSMGSKSFSFNNVVTFTTLINGYCKAGRVDG	600
Sbjct	624	GIVPDTITYSSMIDGLCKQSRLEATQMFDSMGSKSFSFNNVVTFTTLINGYCKAGRVDG	683
Query	601	LELFCEMGRGIVANAITYITLICGFRKVGNGINGALDIFOEMISSGVYPTITIRNMLTG	660
Sbjct	684	LELFCEMGRGIVANAITYITLICGFRKVGNGINGALDIFOEMISSGVYPTITIRNMLTG	743
Query	661	LWSKEELKRAVAMLEKLQMSM	681
Sbjct	744	LWSKEELKRAVAMLEKLQMSM	764

- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against SEQ 6 from Brown provisional No. 2 (60/305,363)**

Score = 974 bits (2517), Expect = 0.0

Identities = 510/688 (74%), Positives = 568/688 (82%), Gaps = 48/688 (6%)

## Group 5

Query	1	MLARVCGFKCSPSSPAESARLFCTRSIRDTLAKASGESCEAGFGGSEKLKQSGFHEIKGL	60
		MLARV SSSPA SAARLFCTRSIR LAK S + E+GFGGESLKL+SGFHEIKGL	
Sbjct	1	MLARVYRSGSSSPAVSAARLFCTRSIRHALAKKSRDG-ESGFGGESLKLKSGFHEIKGL	59
Query	61	EDAIDLFSMDLRSRPLPSVVDPFCKLMGVVVRMERPDVLISLYQMKMERKQIRCDIYSFNIL	120
		EDAIDL F DM+RSRPLPSV+DFCKLMGVVVRM R D+VISL++KME +++ C+ YSF IL	
Sbjct	60	EDAIDLFGDMVRSRPLPSVIDPFCKLMGVVVRMGRLDVVISLHRKMEMRRVPCNAYSFTIL	119
Query	121	IKCFCSCKLPFALSTFGKITKGLHDPDVVTFITLLHGLCVEDRVSEALDFFHQMFETTC	180
		+KCFCSCKLPFALSTFGKITKGL FH	
Sbjct	120	MKCFCSCKLPFALSTFGKITKGL-----FH-----	145
Query	181	RPNVVTFTTLMNGLCREGRIVEAVALDRMEDGLQPTQITYGTIVDMCKKGDTVSALN	240
		P VVTF+TL++GLC E RI EA+ L +M + P +T+ T+++G+C++G V A+	
Sbjct	146	-PTVVTFSTLLHGLCEDRISEALDLFHQMCK---PNNVVTFTTLMNGLCREGRIVEAVA	200
Query	241	LLRKMEEVSHIIPNNVIYSAIIDSCLKDGRHSDAQNLFTEMQEGK-IFPDLFY-----N	294
		LL +M E + PN + Y I+D +CK G A NL +M+E I P++ +	
Sbjct	201	LLDRMLE-DGLQPNQITYGTIVDMCKMGDTVSALNLLRKMEEVSHIKPNNVIWPLERRT	259
Query	295	SMIVGFCSSGRWSDAEQLLOEMLERK-ISPDPVVTYNALINAFVKEGKFFEAEEELYDEMPL	353
		M I GFCSSGRWS+A-QLLQOEMLERK ISPDPVVTYNALINAFVKEGKFFEAEEELYDEMPL	
Sbjct	260	CMINGFCSSGRWSEAQQLLOEMLERKKISPDPVVTYNALINAFVKEGKFFEAEEELYDEMPL	319
Query	354	RGIIPNTITYSSMIDGFCKQNRDLAAEHMFYLMATKGCSPNLTITFNTLIDGYCGAKRID	413
		RGIIP+TITYSSMIDGFCKQNRDLAAEHMFYLMATKGCSP++ITFNTLI GYC AKR+DD	
Sbjct	320	RGIIPSTITYSSMIDGFCKQNRDLAAEHMFYLMATKGCSPDIITFNTLIAGYCRAKRVDD	379
Query	414	GMELLHEMTETGLVADTTTYNTLIHGFIYLVGDLNAAALDLLOEMISSGLCPDIVTCDTLDD	473
		G++LLHEMT E GLVA+T TY TLIHG F VGDNLAA DLLQEM+SSG+CP++VTC+TLDD	
Sbjct	380	GIKLLHEMT EAGLVANTITYTTLIHGFCQVGDNLAAQDLLOEMISSGVCNNVTCNTLDD	439
Query	474	GLCDNGKLKDALEMFKVMQSKKDLDAHPFNGVEPVDQTYNINISGLINEGKFLEAEEL	533
		GLCDNGKLKDALEMFK MQSK D-DASHPFNGVEPVDQTYNINISGLINEGKFLEAEEL	
Sbjct	440	GLCDNGKLKDALEMFKAMQSKMDIDASHPFNGVEPVDQTYNINISGLINEGKFLEAEEL	499
Query	534	YEEMPHRGIVPDTITYSSMIDGLCKQSRLEATQMFDSMGSKSFSPNNVVTFTTLINGYCK	593
		YEEMPHRGIVPDTITY+S+I GLCKQSRLEATQMFDSMGSKSFSPNNVVTFTTLINGYCK	
Sbjct	500	YEEMPHRGIVPDTITYNSVIHGLCKQSRLEATQMFDSMGSKSFSPNNVVTFTTLINGYCK	559
Query	594	AGRVDDGLELFCMGRRGIVANAITYITLICGFRKVGNGINGALDIFOEMISSGVYPDTIT	653
		AGRVDDGLELFCMGRRGIVANAITYITLI GFRKVGNGINGALDIFOEM++SGVYPDTIT	
Sbjct	560	AGRVDDGLELFCMGRRGIVANAITYITLIHGFRKVGNGINGALDIFOEMASGVYPDTIT	619
Query	654	IRNMLTGLWSKEELKRAVAMLEKLQMSM 681	
		IRNMLTGLWSKEELKRAVAMLE LQMS+	
Sbjct	620	IRNMLTGLWSKEELKRAVAMLEDLQMSV 647	

- SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 1 from Brown provisional No. 3 (60/308,736)

## Group 5

Score = 521 bits (1341), Expect = 2e-145

Identities = 261/395 (66%), Positives = 311/395 (78%), Gaps = 1/395 (0%)

```

Query 288 PDLETYSNMIVGFCSSGRWSDAEQLLEMLERKISPDVVYTNALINAFVKEGKFFAEEL 347
      P++ T+ +++ G C GR +A LL M+E + P+ +TY +++ K G A L
Sbjct 4 PNVVTTTTLMNGLCREGRVVEAVALDRMVEDGLQPNQITYGTIVDGMCKMGDTVSALNL 63

Query 348 YDEMLPRGII-PNTITYSSMIDGFCCKQNRDLAAEHMFYLMATKGCSPNLITFNTLIDGYC 406
      +M I P+ + YS++IDG K R A+++F M KG P+++T++ +I+G+C
Sbjct 64 LRKMEELSHIKPDVVIYSAIDGLWKDGRHTDAQNLFIEMQDKGIFPDIVTYSMINGFC 123

Query 407 GAKRIDDGEMELHMETETGLVADTTTYNTLIHGFIYLVGDLNLAALDLQEMISSGLCPDIV 466
      + + + LL EM + D T++ LI+ GD LN+A DLLQEMISSG+CP++V
Sbjct 124 SSGKWSEAEQRLLEMLVRKISPDVVTFSGLINALVKEGDLNSAQDLLQEMISSGVCNVV 183

Query 467 TCDTLLDGLCDNGKLKDALEMEFKVMQSKKDLDAHPNGVEPDVQTYNIIISGLINEGK 526
      TC+TLLDGLCD GKLDKDALEMEFK MQKS D+DA+H FNGVEPDVQTYNIIISGLINEGK
Sbjct 184 TCNTLLDGLCDRGLKDALEMEFKAMQKSMMDIDATHAFNGVEPDVQTYNIIISGLINEGK 243

Query 527 FLEAEELYEEMPHRGIVPDTITYSSMIDGLCKQSRLEATQMFDSMGSKSFSPNVVTF 586
      FLEAEELYEEMPHRGIVPDT+TYSSMI+GLCKQSRLEATQMFDSMGSKSFSPN+VTF T
Sbjct 244 FLEAEELYEEMPHRGIVPDTVITYSSMINGLCKQSRLEATQMFDSMGSKSFSPNIVTFNT 303

Query 587 LINGYCKAGRVDDGLELFCMGRRGIVANAITYITLICGFRKVGNGINGALDIFQEMISSG 646
      LI GYCKAG VDDGLELFCMGRRGIVANAITYITLI GFRKVGNGING+LDIFQEMISSG
Sbjct 304 LITGYCKAGMVDGLELFCMGRRGIVANAITYITLIRGFRKVGNGINGSLDIFQEMISSG 363

Query 647 VYPDTITIRNMLTGLWSKEELKRAVAMLEKLQMS 681
      VYPDTITIRNMLTGLWSKEELKRA+AMLE+LQMSM
Sbjct 364 VYPDTITIRNMLTGLWSKEELKRALAMLEELQMS 398
    
```

Score = 394 bits (1012), Expect = 2e-107

Identities = 208/404 (51%), Positives = 265/404 (65%), Gaps = 22/404 (5%)

```

Query 180 CRPNVVTFTTLMNGLCREGRIVEAVALDRMMDGLQPTQITYGTIVDGMCKKGDVTSAL 239
      C+PNVVTFTTLMNGLCREGR+VEAVALDRM+EDGLQPTQITYGTIVDGMCK GDVTSAL
Sbjct 2 CRPNVVTFTTLMNGLCREGRVVEAVALDRMVEDGLQPNQITYGTIVDGMCKMGDTVSAL 61

Query 240 NLLRKMEEVSHIIPNVVIYSAIDSLCKDGRHSDAQNLFTEMQEKGIFPDFTYNSMIVG 299
      NLLRKMEE+SHI P+VVIYSAIID L KDGRH+DAQNLF EMQ+KGIFPD+ TY+ MI G
Sbjct 62 NLLRKMEELSHIKPDVVIYSAIDGLWKDGRHTDAQNLFIEMQDKGIFPDIVTYSMING 121

Query 300 FCSSGRWSDAEQLLEMLERKISPDVVYTNALINAFVKEGKFFAEELYDEMLPRGIIPN 359
      FCSSG+WS+A++LLQEML RKISPDVV++ LINA VKEG A++L EM+ G+ PN
Sbjct 122 FCSSGKWSEAEQRLLEMLVRKISPDVVTFSGLINALVKEGDLNSAQDLLQEMISSGVCN 181

Query 360 TITYSSMIDGFCCKQNRDLAAEHMFYLM-----ATKGCSPNLITFNTLIDGYCGA 408
      +T +++++DG C + +L A MF M A G P++ T+N LI G
Sbjct 182 VVTCNTLLDGLCDRGLKDALEMEFKAMQKSMMDIDATHAFNGVEPDVQTYNIIISGLINE 241
    
```

## Group 5

```

Query 409 KRIDGDMELLHEMTETGLVADTTTNTLIHGFYLVGDLNAAALLQEMISSGLCPDIVTC 468
      + + EL EM G+V DT TY+++I+G L+ A + M S P+IVT
Sbjct 242 GKFLAEAEELYEEMPHRGIVPDTVTYSSMINGLCKQSRLEATQMFDSMGSKSFSPNIVTF 301

Query 469 DTLLDGLCDNGKLKDALEMFKVMQSKKDLASHPFNGVEPVDQTYNIIISGLINEGKFL 528
      +TL+ G C G + D LE+F M + G + TY LI G G
Sbjct 302 NTLITGYCKAGMVDDGLELFCCEMGR-----RGIVANAITYITLIRGFRKVGNGIN 350

Query 529 EAEELYEEMPHRGIVPDTITYSSMIDGLCKQSRLEATQMFDSM 572
      + ++++EM G+ PDTIT +M+ GL + L A M + +
Sbjct 351 GSLDIFQEMISSGVYPTTITIRNMLTGLWSKEELKRALAMLEEL 394
  
```

Score = 300 bits (767), Expect = 6e-79

Identities = 166/395 (42%), Positives = 229/395 (57%), Gaps = 48/395 (12%)

```

Query 147 PDVVTTTLLHGLCEVDREVSEALDFFHQMFTTCRPNVVTFTLLMNGLCREGRIVEAVAL 206
      P+VVTTTLL++GLC E RV EA+ +M E +PN +T+ T+++G+C+ G V A+ L
Sbjct 4 PNVVTTTLLMNGLCREGRVVEAVALDRMVDEGLQPNQITYGTIVDGMCKMGDTVSALNL 63

Query 207 LDRMME-DGLQPTQITYGTIVDGMCKKGDTSVSNLLRKMEEVSHIIPNVVVISAIIDSL 265
      L +M E ++P + Y I+DG+ K G A NL +M++ I P++V YS +I+
Sbjct 64 LRKMEELSHIKPDVVVISAIIDGLWKDGRHTDAQNLFIEMQD-KGIFPDIVTYSCEMNGF 122

Query 266 CKDGRHSDAQNLFTEMQEKGIFFDLFTYNSMIVGFCSSGRWSDAEQLLQEMLE----- 318
      C G+ S+AQ L EM + I PD+ T++ +I G + A+ LLQEM+
Sbjct 123 CSSGKWSEARLLQEMLVKISPDVVTFSLGALNALVKEGDLNSAQDLLQEMISSGVCPNV 182

Query 319 -----RKISPDVVVTYNALINAFVKEG 339
      + PDV TYN LI+ + EG
Sbjct 183 VTCNTLLDGLCDRGLKDALEMFKAMQKSMMDIDATHAFNGVEPVDQTYNIIISGLINEG 242

Query 340 KFFEAEELYDEMLPRGIIPNTITYSSMIDGFCQNRDLAAEHMFYLMATKGCSPNLITFN 399
      KF EAEELY+EM RGI+P+T+TYSSMI+G CKQ+RLD A MF M +K SPN++TFN
Sbjct 243 KFLAEAEELYEEMPHRGIVPDTVTYSSMINGLCKQSRLEATQMFDSMGSKSFSPNIVTFN 302

Query 400 TLIDGYCGAKRIDGDMELLHEMTETGLVADTTTNTLIHGFYLVGDLNAAALLQEMISS 459
      TL+ GYC A +DDG+EL EM G+VA+ TY TL+ GF VG++N +LD+ QEMISS
Sbjct 303 TLITGYCKAGMVDDGLELFCCEMGRGIVANAITYITLIRGFRKVGNGINGSLDIFQEMISS 362

Query 460 GLCPDIVTCDTLLDGLCDNGKLKDALEMFKVMQKS 494
      G+ PD +T +L GL +LK AL M + +Q S
Sbjct 363 GVYPTTITIRNMLTGLWSKEELKRALAMLEELQMS 397
  
```

Score = 216 bits (551), Expect = 7e-54

Identities = 120/392 (30%), Positives = 214/392 (54%), Gaps = 13/392 (3%)



## Group 5

Query	77	PSVVDFCKLMGVVVRMERPDVLVISLYQKMERKQIRCDIYSFNILIKCFCSCSKLPFALST	136
Sbjct	4	P+VV F LM + R R ++L +M ++ + ++ ++ C AL+ PNVVFTTLLMNGLCREGRVVEAVALLDRMVEDGLQPNQITYGTIVDGMCKMGDTVSALNL	63
Query	137	FGKITKLG-LHPDVVFTTLLHGLCVEDRVSEALDFFHQMFETTCRPNVVFTTLLMNGLC	195
Sbjct	64	K+ +L + PDVV ++ ++ GL + R ++A + F +M + P++VT++ ++NG C LRKMEELSHIKPDVVIYSIAIDGLWKDGRHTDAQNLFIEMQDKGIFPDIVTYS CMINGFC	123
Query	196	REGRIEAVALLDRMMDGLQPTQITYGTIVDGMCKKGDTVSALNLLRKMEEVSHIIPNV	255
Sbjct	124	G+ EA LL M+ + P +T+ +++ + K+GD SA +LL++M S + PNV SSGKWSEAQRLLEQMLVRKISPDVVTFSGLINALVKEGDLNSAQDLLQEMIS-SGVC PN	182
Query	256	VIYSIAIDSLCKDGRHSDAQNLFTEMQE-----KGIFPDFTYNSMIVGFCSSG	304
Sbjct	183	V + ++D LC G+ DA +F MQ+ G+ PD+ TYN +I G + G VTCNTLLDGLCDRGKLDALMFAMQKSMMDIDATHAFNGVEPDVQTYNIIISGLINEG	242
Query	305	RWSDAEQLLQEMLERKISPDVVTYNALINAFVKEGKFFEAELYDEMLPRGIIPNTITYS	364
Sbjct	243	++ +AE+L +EM R I PD VTY+++IN K+ + EA +++D M + PN +T++ KFLEAEELYEEMPHRGIVPDTVITYSSMINGLCKQSRLEATQMFDSMGSKSFSPNIVTFN	302
Query	365	SMIDGFCQNRDLAAEHMFYLMATKGCSPNLITENTLIDGYCGAKRIDDGEMELHEMTET	424
Sbjct	303	+I G+CK +D +F M +G N IT+ TLI G+ I+ +++ EM + TLITGYCKAGMVDGLELFCFEMGRRGIVANAITYITLIRGFRKVGNGINGSLDIFQEMISS	362
Query	425	GLVADTTTYNTLIHGFLVGLDNLALDLLQEM	456
Sbjct	363	G+ DT T ++ G + +L AL +L+E+ GVYPTTITIRNMLTGLWSKEELKRALAMLEEL	394

Score = 193 bits (491), Expect = 6e-47

Identities = 109/371 (29%), Positives = 193/371 (52%), Gaps = 11/371 (2%)

Query	62	DAIDLFSDMLRSRPLSPVDFCKLMGVVVRMERPDVLVISLYQKMER-KQIRCDIYSFNIL	120
Sbjct	24	+A+ L M+ P+ + + ++ + +M ++L +KME I+ D+ ++ + EAVALLDRMVEDGLQPNQITYGTIVDGMCKMGDTVSALNLLRKMEEELSHIKPDVVIYSIAI	83
Query	121	IKCFCSCSKLPFALSTFGKITKLGHPDVVFTTLLHGLCVEDRVSEALDFFHQMFETT	180
Sbjct	84	I + A + F ++ G+ PD+VT++ ++G C + SEA +M IDGLWKDGRHTDAQNLFIEMQDKGIFPDIVTYS CMINGFCSSGKWSEAQRLLEQMLVRKI	143
Query	181	RPNVVFTTLLMNGLCREGRIVEAVALLDRMMDGLQPTQITYGTIVDGMCKKGDTVSALN	240
Sbjct	144	P+VVTF+ L+N L +EG+ A LL M+ G+ P +T T++DG+C +G AL SPDVVTFSGLINALVKEGDLNSAQDLLQEMISSGVC PNVTTCNTLLDGLCDRGKLDAL	203
Query	241	LLRKME-----EVSH----IIPNVVIYSIAIDSLCKDGRHSDAQNLFTEMQEKGIFPD	290
Sbjct	204	+ + M+ + +H +G+ P+V Y+ +I L +G+ +A+ L+ EM +GI PD MFKAMQKSMMDIDATHAFNGVEPDVQTYNIIISGLINEGKFLEAEELYEEMPHRGIVPDT	263
Query	291	FTYNSMIVGFCSSGRWSDAEQLLQEMLERKISPDVVTYNALINAFVKEGKFFEAELYDE	350
Sbjct	264	TY+SMI G C R +A Q+ M + SP++VT+N LI + K G + EL+ E VTYSSMINGLCKQSRLEATQMFDSMGSKSFSPNIVTFNTLITGYCKAGMVDGLELFC	323

## Group 5

Query 351 MLPRGLIPNTITYSSMIDGFCKQNRDLAAEHMFYLMATKGCSPNLITFNTLIDGYCGAKR 410  
 M RGI+ N ITY ++I GF K ++ + +F M + G P+ IT ++ G +  
 Sbjct 324 MRRRGIVANAITYITLIRGFRKVGNGSLDIFQEMISSGVYPDITITRNMLTGLWSKEE 383

Query 411 IDDGMEELLHEM 421  
 + + +L E+  
 Sbjct 384 LKRALAMLEEL 394

Score = 118 bits (296), Expect = 3e-24  
 Identities = 78/282 (27%), Positives = 130/282 (46%), Gaps = 12/282 (4%)

Query 52 SGFHEIKGLEDAIDLFSDMLRSRPLSPVDFCKLMGVVVRMERPDLVISLYQKMERKQIR 111  
 +GF +A L -ML + P VV F L+ +V+ + L Q+M +  
 Sbjct 120 NGFCSSGKWSEAQRLLQEMLRKISPDVVTFSGLINALVKEGDLNSAQDLLQEMISSGVC 179

Query 112 CDIYSENLILKPCFSCSKLPFALSTFGKITKL-----GLHPDVVFTTLLHGLC 160  
 ++ + N L+ C KL AL F + K G+ PDV T+ L+ GL  
 Sbjct 180 PNVVTCNTLLDGLCDRGLKDALEMFKAMQKSMMDIDATHAFNGVEPDVQTYNILISGLI 239

Query 161 VEDRVSEALDFHQMFEETTCRPNVVTFTTLMNGLCREGRIVEAVALDRMDEGLQPTQI 220  
 E + EA + + +M P+ VT++++NGLC++ R+ EA + D M P +  
 Sbjct 240 NEGKPLEAEELYEEMPHRGIVPDVTVYSSMINGLCKQSRLEATQMFDSMGSKSFSFNIV 299

Query 221 TYGTIVDGMCKGDTVSALNLLRKMEEVSHIIPNVVIYSAIIDSCKDGRHSDAQNLFT 280  
 T+ T++ G CK G L L +M I+ N + Y +I K G + + ++F E  
 Sbjct 300 TFNTLITGYCKAGMVDGGLFCEMGRRG-IVANAITYITLIRGFRKVGNGSLDIFQE 358

Query 281 MQEKGIFPDLFYTNMIVGFCSSGRWSDAEQLLQEMLERKIS 322  
 M G++PD T +M+ G S A +L+E+ +S  
 Sbjct 359 MISSGVYPDITITRNMLTGLWSKEELKRALAMLEELQMSMVS 400

- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 2 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 3 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 4 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 5 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found

## Group 5

- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 6 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 7 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 8 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 9 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 10 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 11 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 12 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 13 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 14 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 15 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 16 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found

## Group 5

- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 17 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 18 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 19 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 20 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 21 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 22 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 23 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 24 from Brown provisional No. 3 (60/308,736)**

Score = 1179 bits (3049), Expect = 0.0

Identities = 594/683 (86%), Positives = 628/683 (91%), Gaps = 6/683 (0%)

Query	1	MLARVCGFKSSSPAESAARLFCTRSIRDTLAKAS--GESCEAGFGGESLKLQSGFHEIK	58
		MLARVC F+ SSS + SAAR FCT SIR LA+ S GES EAGF GESLKL+SG +EIK	
Sbjct	1	MLARVCFRESSSSSSVSAARFFCTGSIRHALAEKSRDGESEAGFRGESLKLRSRGSYEIK	60
Query	59	GLEDAIDLFSMDLRSRPLPSVVD FCKLMGVVVRMERPDVLISLYQKMERKQIRCDIYSFN	118
		GLEDAIDLFSMDLRSRPLPSV+DF KLMG VVRMERPDVLISLYQKMERKQIRCDIYSF	
Sbjct	61	GLEDAIDLFSMDLRSRPLPSVIDFNKLMGAVVRMERPDVLISLYQKMERKQIRCDIYSFT	120
Query	119	ILIKCFCSCSKLPALSTFGKITKLGLHPDVVTF T TLLHGLCVDREVSEALDFFHQMFET	178
		ILIKCFCSCSKLPALSTFGK+TKLGLHPDVVTF T TLLHGLC++ RVSEALD FHQ+	
Sbjct	121	ILIKCFCSCSKLPALSTFGKLTKLGLHPDVVTF T TLLHGLCLDHRVSEALDLFHQI---	177

## Group 5

Query	179	TCRPNVVTFTTLMNGLCREGRIVEAVALLDRMMEDGLQPTQITYGTIVDGMCKKGDVSA	238
		CRP+V+TFTTLMNGLCREGR+VEAVALLDRM+E+GLQP QITYGT VDGCKK GDVSA	
Sbjct	178	-CRPDLVLTFTTLMNGLCREGRVVEAVALLDRMVENGLOPQITYGTFFVDGMCKMGDTVSA	236
Query	239	LNLLRKMEEVSHIIPNVVIYSAIIDSCKDGRHSDAQNLFTEMQEKGIFPDFTYNSMIV	298
		LNLLRKMEE+SHIIPNVVIYSAIID LCKDGRHSD+ NLF EMQ+KGIFP++ TYN MI	
Sbjct	237	LNLLRKMEEISHIKPNVVIYSAIIDGLCKDGRHSDSHNLFTEMQDKGIFPNIVTYNCMIG	296
Query	299	GFCSSGRWSDAEQLLQEMLERKISPVDVTYNALINAFVKEGKFFEAELYDEMLPRGIIP	358
		GFC SGRWS A++LLQEMLERKISP+VVTYNALINAFVKEGKFFEA ELYDEMLPRGIIP	
Sbjct	297	GFCISGRWSAAQRLLQEMLERKISPVDVTYNALINAFVKEGKFFEAELYDEMLPRGIIP	356
Query	359	NTITYSSMIDGFCQNRDLAAEHMFYLMATKGCSPNLITFNTLIDGYCGAKRIDDMELL	418
		NTITY+SMIDGFCQ+RLDAE MFYLMATKGCSP++ TF TLDGYCGAKRIDDMELL	
Sbjct	357	NTITYNSMIDGFCQNRDLAAEDMFYLMATKGCSPDVFTFTLIDGYCGAKRIDDMELL	416
Query	419	HEMTETGLVADPTTYNTLIHGFYLVGDLNAAALDLQEMISSGLCPDIVTCNTLLDGLCDN	478
		HEM GLVA+T TYNTLIHGF LVGDLNAAALDL Q+MISSG+CPDIVTC+TLLDGLCDN	
Sbjct	417	HEMPRRGLVANTVTYNTLIHGFCLVGDNLNAAALDLQMISSGVCPIVTCNTLLDGLCDN	476
Query	479	GKLDKDALEMFVKQKSKDLASHPFNGVEPDVQTYNILISGLINEGKFLAEELYEEMP	538
		GKLDKDALEMFK MQKSK DLDASHPFNGVEPDV TYNILI GLINEGKFLAEELYEEMP	
Sbjct	477	GKLDKDALEMFKAMQKSKMDLDASHPFNGVEPDVLTYNILICGLINEGKFLAEELYEEMP	536
Query	539	HRGIVPDTITYSSMIDGLCKQSRLEATQMFDSMGSKSFPNVVFTTTLINGYCKAGRVD	598
		HRGIVPDTITYSSMIDGLCKQSRLEATQMF SMGSKSFPNVVTF TLINGYCKAGRVD	
Sbjct	537	HRGIVPDTITYSSMIDGLCKQSRLEATQMFVSMGSKSFPNVVFTTLINGYCKAGRVD	596
Query	599	DGLELFCMGRRGIVANAIYITLICGFRKVGNGINGALDIFQEMISSGVYPDITIRNML	658
		DGLELFCMGRRGIVA+AI YITLI GFRKVGNGINGALDIFQEMISSGVYPDITIRNML	
Sbjct	597	DGLELFCMGRRGIVADAIYITLIYGRKVGNGINGALDIFQEMISSGVYPDITIRNML	656
Query	659	TGLWSKEELKRAVAMLEKLQMSM 681	
		TG WSKEEL+RAVAMLE LQMS+	
Sbjct	657	TGFWKSKEELERAVAMLEDLQMSV 679	

- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 25 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 26 from Brown provisional No. 3 (60/308,736)**

Score = 1368 bits (3541), Expect = 0.0  
 Identities = 681/681 (100%), Positives = 681/681 (100%), Gaps = 0/681 (0%)

Query	1	MLARVCGFKCSSPAESAARLFCTRSIRDTLAKASGESCEAGFGGESLKLQSGFHEIKGL	60
		MLARVCGFKCSSPAESAARLFCTRSIRDTLAKASGESCEAGFGGESLKLQSGFHEIKGL	
Sbjct	84	MLARVCGFKCSSPAESAARLFCTRSIRDTLAKASGESCEAGFGGESLKLQSGFHEIKGL	143

## Group 5

Query	61	EDAIDLFSMDLRSRPLPSVDFCKLMGVVVRMERPDVLISLYQKMERKQIRCDIYSFNIL	120
Sbjct	144	EDAIDLFSMDLRSRPLPSVDFCKLMGVVVRMERPDVLISLYQKMERKQIRCDIYSFNIL	203
Query	121	IKCFCSCSKLPALSTFGKITKGLGHPDVVTFITLLHGLCVDREVSEALDFFHQMFETTC	180
Sbjct	204	IKCFCSCSKLPALSTFGKITKGLGHPDVVTFITLLHGLCVDREVSEALDFFHQMFETTC	263
Query	181	RPNVVTFTTLMNGLCREGRIVEAVALDRMMEDGLQPTQITYGTIVDGMCKKGDVTSALN	240
Sbjct	264	RPNVVTFTTLMNGLCREGRIVEAVALDRMMEDGLQPTQITYGTIVDGMCKKGDVTSALN	323
Query	241	LLRKMEEVSHIIPNVVIYSAIIDSLCKDGRHSDAQNLFTEMQEKGIFFDLFTYNSMIVGF	300
Sbjct	324	LLRKMEEVSHIIPNVVIYSAIIDSLCKDGRHSDAQNLFTEMQEKGIFFDLFTYNSMIVGF	383
Query	301	CSSGRWSDAEQLLOEMLERKISPDVVYTINALINAFVKEGKFFEAELYDEMLPRGIIPNT	360
Sbjct	384	CSSGRWSDAEQLLOEMLERKISPDVVYTINALINAFVKEGKFFEAELYDEMLPRGIIPNT	443
Query	361	ITYSSMIDGFCQKQNRDLAAEHMFYLMATKGCSPLNITFTNLIDGYCGAKRIDDMELLHE	420
Sbjct	444	ITYSSMIDGFCQKQNRDLAAEHMFYLMATKGCSPLNITFTNLIDGYCGAKRIDDMELLHE	503
Query	421	MTETGLVADTTTYNTLIHGFIYLVGDLNAAALLQEMISSGLCPDIVTCDTLLDGLCDNGK	480
Sbjct	504	MTETGLVADTTTYNTLIHGFIYLVGDLNAAALLQEMISSGLCPDIVTCDTLLDGLCDNGK	563
Query	481	LKDALEMFKVMQSKKDLDAHPFNGVEPDVQTYNILISGLINEGKFLEAEELYEEMPHR	540
Sbjct	564	LKDALEMFKVMQSKKDLDAHPFNGVEPDVQTYNILISGLINEGKFLEAEELYEEMPHR	623
Query	541	GIVPDTITYSSMIDGLCKQSRLEATQMFDSMGSKSFSPNVVFTTTLINGYCKAGRVDG	600
Sbjct	624	GIVPDTITYSSMIDGLCKQSRLEATQMFDSMGSKSFSPNVVFTTTLINGYCKAGRVDG	683
Query	601	LELFCEMGRGIVANAITYITLICGFRKVGNGINGALDIFOEMISSGVYPTITIRNMLTG	660
Sbjct	684	LELFCEMGRGIVANAITYITLICGFRKVGNGINGALDIFOEMISSGVYPTITIRNMLTG	743
Query	661	LWSKEELKRAVAMLEKLQMSM	681
Sbjct	744	LWSKEELKRAVAMLEKLQMSM	764

- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 27 from Brown provisional No. 3 (60/308,736)**

Score = 974 bits (2517), Expect = 0.0

Identities = 510/688 (74%), Positives = 568/688 (82%), Gaps = 48/688 (6%)

## Group 5

Query	1	MLARVCGFKCSSSPAESARLFCSTRSIRDTLAKASGESCEAGFGGESLKLQSGFHEIKGL	60
		MLARV SSSPA SAARLFCSTRSIR LAK S + E+GFGGESLKL+SGFHEIKGL	
Sbjct	1	MLARVYRSGSSSPAVSARLFCSTRSIRHALAKKSRDG-ESGFGGESLKLRSGFHEIKGL	59
Query	61	EDAIDLFSMDLRSRPLPSVVDPFCKLMGVVVRMERPDVLISLYQMKMERKQIRCDIYSFNIL	120
		EDAIDL F DM+RSRPLPSV+DFCKLMGVVVRM R D+VISL++KME +++ C+ YSF IL	
Sbjct	60	EDAIDLFGDMVRSRPLPSVIDPFCKLMGVVVRMGRLDVVISLHRKMEMRRVPCNAYSFTIL	119
Query	121	IKCFCSCKLPFALSTFGKITKGLHDPDVVTTTLLHGLCVEDRVSEALDFFHQMFETTC	180
		+KCFCSCKLPFALSTFGKITKLG FH	
Sbjct	120	MKCFCSCKLPFALSTFGKITKLG-----FH-----	145
Query	181	RPNVVTFTTLMNGLCREGRIVEAVALDRMMEDGLQPTQITYGTIVDMCKKGDTVSALN	240
		P VVTF+TL++GLC E RI EA+ L +M + P +T+ T+++G+C++G V A+	
Sbjct	146	-PTVVTFSTLLHGLCEDRISEALDLFHQMCK---PNNVVTFTTLMNGLCREGRVVEAVA	200
Query	241	LLRKMEEVSHIIPNNVIYSAIIDSCLKDGRHSDAQNLFTEMQEGK-IPFDLFTY-----N	294
		LL +M E + PN + Y I+D +CK G A NL +M+E I P++ +	
Sbjct	201	LLDRMLE-DGLQPNQITYGTIVDMCKMGDTVSALNLLRKMEEVSHIKPNNVIWPLERRT	259
Query	295	SMIVGFCSSGRWSDAEQLQOEMLERK-ISPDPVVTYNALINAFVKEGKFFEAEEYDEMLP	353
		M I GFCSSGRWS+A-QLLQOEMLERK ISPDPVVTYNALINAFVKEGKFFEAEEYDEMLP	
Sbjct	260	CMINGFCSSGRWSEAQQLQOEMLERKKISPDPVVTYNALINAFVKEGKFFEAEEYDEMLP	319
Query	354	RGIIPNTITYSSMIDGFCQKQNRDLAAEHMFYLMATKGCSPNLTITFNTLIDGYCGAKRID	413
		RGIIP+TITYSSMIDGFCQKQNRDLAAEHMFYLMATKGCSP++ITFNTLI GYC AKR+DD	
Sbjct	320	RGIIPSTITYSSMIDGFCQKQNRDLAAEHMFYLMATKGCSPDIITFNTLIAGYCRAKRVDD	379
Query	414	GMELLHEMETETGLVADTTTYNTLIHGFIYLVGDLNAAALDLLQEMISSGLCPDVICTDILL	473
		G++LLHEMTE GLVA+T TY TLIHG V GDLNAA DLLQEM+SSG+CP++VTC+TLID	
Sbjct	380	GIKLLHEMTEAGLVANTITYTTLIHGFCQV GDLNAAQDLLQEMVSSGVCNNVTCNTLLD	439
Query	474	GLCDNGKLKDALEMFKVMQKSKKDL DASHFPNGVEPDPVQTYNINILISGLINEGKFLEAEEL	533
		GLCDNGKLKDALEMFK MQSK D-DASHFPNGVEPDPVQTYNINILISGLINEGKFLEAEEL	
Sbjct	440	GLCDNGKLKDALEMFKAMQKSKMDIDASHFPNGVEPDPVQTYNINILISGLINEGKFLEAEEL	499
Query	534	YEEMPHRGIVPDTITYSSMIDGLCKQSRLEATQMFDMSGKSFSPNNVVTFTTLINGYCK	593
		YEEMPHRGIVPDTITY+S+I GLCKQSRLEATQMFDMSGKSFSPNNVVTFTTLINGYCK	
Sbjct	500	YEEMPHRGIVPDTITYNSVIHGLCKQSRLEATQMFDMSGKSFSPNNVVTFTTLINGYCK	559
Query	594	AGRVDDGLELFCMGRRGIVANAITYITLICGFRKVGNGINGALDIFOEMISSGVYPDTIT	653
		AGRVDDGLELFCMGRRGIVANAITYITLI GFRKVGNGINGALDIFOEM++SGVYPDTIT	
Sbjct	560	AGRVDDGLELFCMGRRGIVANAITYITLIHGFRKVGNGINGALDIFOEMMASGVYPDTIT	619
Query	654	IRNMLTGLWSKEELKRAVAMLEKLQMSM 681	
		IRNMLTGLWSKEELKRAVAMLE LQMS+	
Sbjct	620	IRNMLTGLWSKEELKRAVAMLEDLQMSV 647	

- SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 28 from Brown provisional No. 3 (60/308,736)

## Group 5

- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 29 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 30 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 31 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 32 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 33 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 34 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 35 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 36 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 37 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 38 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 39 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found



## Group 5

- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 40 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 41 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 42 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 43 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found